



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 123519

TO: Christopher Yaen
Location: REM/3A20/3C18
Art Unit: 1642
June 4, 2004

Case Serial Number: 09/700770

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

STIC-Biotech/ChemLib

193519

From: Yaen, Christopher
Sent: Wednesday, June 02, 2004 10:33 AM
To: STIC-Biotech/ChemLib
Subject: 09700770

could you please search seq id 7, 8, and 9

thanks

Chris

Christopher Yaen
US Patent Office
Art Unit 1642
571-272-0838
REM 3A20
REM 3C18

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:07:29 ; Search time 16.6872 Seconds
(without alignments)
1966.411 Million cell updates/sec

Title: US-09-700-770-9

Perfect score: 502

Sequence: 1 MKLALLGLCVALSAAAA.....QAVGAVKALKALGALTVEG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacterioph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	44.8	94	11	Q8CJC6
2	88	17.5	255	16	Q82LN6
3	83.5	16.6	281	16	Q8FST3
4	82.5	16.4	247	16	Q9K3G4
5	82.5	16.4	694	16	Q98CR1
6	81	16.1	496	10	Q9SU83
7	80	15.9	148	16	Q9XW23
8	79	15.7	136	16	Q82R50
9	77.5	15.4	229	16	Q7WJ56
10	77.5	15.4	229	16	Q7WA34
11	77.5	15.4	229	16	Q7VYAI
12	77.5	15.4	601	16	Q86691
13	77	15.3	453	17	Q8THL0
14	76	15.1	355	16	Q8UAI4
15	76	15.1	699	16	Q9ABL0
16	76	15.1	889	16	Q8G4X4

17 75.5 15.0 459 16 Q9ZL6 streptomyc
18 75.5 15.0 496 16 Q8G3S5 bifidobacte
19 75.5 15.0 544 17 Q9YEG2 aeropyrum p
20 75.5 15.0 667 16 Q8XRM8 ralistonia s
21 75 14.9 299 16 Q89XU3
22 75 14.9 355 2 Q8RPK5 corynebacte
23 75 14.9 370 16 Q89H46 bradyrhizob
24 75 14.9 463 11 Q8C313 mus musculu
25 74 14.7 611 16 Q9L0K1 streptomyc
26 73.5 14.6 119 5 Q86DI1 leishmania
27 73.5 14.6 331 17 Q9HNI9 halobacteri
28 73.5 14.6 358 16 Q8NQ28 corynebacte
29 73.5 14.6 389 16 Q8EJ01
30 73.5 14.6 1468 5 Q9GUB5
31 73 14.5 317 16 Q8D48 rhizobium l
32 73 14.5 429 16 Q825M1 streptomyc
33 73 14.5 502 16 Q9I5I2 pseudomonas
34 73 14.5 542 10 Q8GYA1
35 73 14.5 584 16 Q9AAR5 caulobacter
36 73 14.5 620 16 Q7WL37 bordetella
37 73 14.5 620 16 Q7W7Q0
38 73 14.5 1279 5 Q7VVR87
39 73 14.5 240 2 Q84CV5
40 72.5 14.4 373 5 Q7WYC1 gamma-prote
41 72.5 14.4 384 16 Q88KE1
42 72.5 14.4 421 2 Q93I77
43 72.5 14.4 482 5 Q9BHF9
44 72.5 14.4 616 16 Q7W2M5 bordetella

ALIGNMENTS

RESULT 1

Q8CJC6 PRELIMINARY; PRT; 94 AA.
ID Q8CJC6
AC Q8CJC6;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE UGRF2 type B.
GS SCGB3A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22326074; PubMed=12438750;
RA Nini T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodasai A., Zimonjic D.B., Keck-Waggoner C.L., Popescu N.C., Kimura S.;
RT "Cloning, expression, and chromosomal localization of the mouse gene (Sc3a1, alias Ugrp2) that encodes a member of the novel uteroglobin-related protein gene family.";
RT Cytogenet. Genome Res. 97:120-127(2002).
DR EMBL: AF313457; AAN63238.1; --
DR MGD: MGI:1915912; Scgb3a1.
SQ SEQUENCE 94 AA; 9578 MW; 7C84B908A6365B59 CRC64;

Query Match 44.8%; Score 225; DB 11; Length 94;
Best Local Similarity 57.3%; Pred. No. 2e-13;
Matches 51; Conservative 14; Mismatches 20; Indels 4; Gaps 2;
QY 17 SAAPFLVGSAPVQAPVAALSAEAAAGAGTIAN-PLGTINPLKLLSLGIPVNHLEGS 75
Db 9 SVAFEMDSLAKPAVEPVAAALAPAAEAVAGVPSPLSHLALRFLILASGMGIPDLLEGS 68
QY 76 OKCAEVLGPQAVGAVKALKALGALTVEG 104
Db 69 RKCVELGPEAVGAV---KSLGLVLTWFG 94

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RESULT 2
ID Q82LNG PRELIMINARY; PRT; 255 AA.
AC Q82LNG;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative methionine aminopeptidase.
GN SAV1974.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
[1]
SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RA "genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
[2]
SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RA "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL: AP005029; BAC69685.1; -
DR GO: GO:004239; F:methionyl aminopeptidase activity; IEA.
DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000994; Peptidase M24.
DR InterPro: IPR002467; Pept M24A MAP1.
DR InterPro: IPR001714; Pept M24 MAP.
DR Pfam: PF00557; Peptidase M24; 1.
DR PRINTS: PR00599; MAPEPTIDASE.
DR TIGRPFAMs: TIGR00500; met_pdase_I; 1.
DR Aminopeptidase; Complete proteome.
KW
SQ SEQUENCE 255 AA; 26727 MW; 0C41CD3010F855A3 CRC64;

Query Match 17.5%; Score 88; DB 16; Length 255;
Best Local Similarity 31.6%; Pred. No. 2,7;
Matches 31; Conservative 16; Mismatches 19; Indels 32; Gaps 6

Qy 7 IGLCVA---LSCSSAAFLVGSKVPVPALE-----SAAEAGA--GTIANPL 51
Db 99 LDLAVARGGVADRAISFLVGKARP-AESVAMIEATERALAAAGIAAKPGARIGDLSHAI 157
Qy 52 GTLNPLKLLSLGIPVNHLEIGSKVCVAELGPQAVGA 89
Db 158 GT-----VLSKAGVPIN-----TEFGCHGIGS 179

RESULT 3
Q8FST3 PRELIMINARY; PRT; 281 AA.
AC Q8FST3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN CE0299.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
[1]
SEQUENCE FROM N.A.

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DE Putative membrane protein.
GN BP1449.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
EA Harris D.E., Holden M.T.G., Churcher C.M., Harris B., Quail M.A.,
RA Cerdano-Tarraga A.M., Temple L., James K., Basham D., Cherevach I.,
RA Achtman M., Aikin R., Baker S., Basham D., Cronin A., Davis P., Doggett J.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
EA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RESULT 5
Q98CR1 PRELIMINARY; PRT; 694 AA.
ID Q98CR1
AC Q98CR1
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein mlf5043.
GN Mlf5043.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
EA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti";
RL DNA Res. 7:331-338(2000).

EMBL: AP003005; BAB51560.1; --
DR GO: GO:000524; F:ATP binding; IEA.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0004812; F:RNA ligase activity; IEA.
DR GO: GO:0006418; P:amino acid activation; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR003781; CoA-binding.
DR InterPro: IPR005811; CoA-binding.
DR InterPro: IPR001412; tRNA-synt 1.
DR Pfam: PF02629; CoA-binding; 1.
DR PROSITE: PS00178; AA TRNA LIGASE I; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 694 AA; 73126 MW; 19E4978531DC6C CRC64;

Query Match 16.4%; Score 82.5; DB 16; Length 694;
Best Local Similarity 33.3%; Pred. No. 25;
Matches 33; Conservative 11; Mismatches 42; Indels 13; Gaps 4;
QY 3 LAALGLCVALS...AKVPAQVVALESAAEAGATLANPLGLTNP-----L 57
Db 438 MVPLFGISEAMDAGAAFGIWAEPQAPVDV--SAAGAAGG-----GHVTFDEAEA 489
QY 58 KLLLSGIGIPVNHLEIGSKVCVAELGPAQVAVKALKAL 96
Db 490 KARLIKAGLPVKGKAGNAVEAVISSNALGFPVVALKAL 528

RESULT 6
Q9SU83 PRELIMINARY; PRT; 496 AA.
ID Q9SU83
AC Q9SU83
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nucleotide mismatch between the two sequences for 36 nt

DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000515; BFD transp.
DR Pfam: PF00528; BFD transp; 2.
KW Complete proteome.
SQ SEQUENCE 601 AA; 61216 MW; 78601FCSAB2DCB9C CRC64;

Query Match 15.4%; Score 77.5; DB 16; Length 601;
Best Local Similarity 30.7%; Pred. No. 63;
Matches 42; Conservative 10; Mismatches 48; Indels 37; Gaps 4;
QY 3 LAALGLCVALS...AKVPAQVVALESAAEAGATLANPLGLTNP-----L 57
Db 438 MVPLFGISEAMDAGAAFGIWAEPQAPVDV--SAAGAAGG-----GHVTFDEAEA 489
QY 58 KLLLSGIGIPVNHLEIGSKVCVAELGPAQVAVKALKAL 96
Db 490 KARLIKAGLPVKGKAGNAVEAVISSNALGFPVVALKAL 528

RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Rosa M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AL079344; CAB45338.1; --
DR EMBL: AL161575; CAB79726.1; --
DR PIR: T09931; T09931.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004551; F:nucleotide diphosphatase activity; IEA.
DR InterPro: IPR002591; Phosphodiesterase.
DR Pfam: PF01663; Phosphodiesterase; 1.
KW Hydrolase.
SQ SEQUENCE 496 AA; 54678 MW; 8DC2BA346121D732 CRC64;

Query Match 16.1%; Score 81; DB 10; Length 496;
Best Local Similarity 41.3%; Pred. No. 24;
Matches 26; Conservative 14; Mismatches 17; Indels 6; Gaps 3;
QY 6 LLGLCVALS...AKVPAQVVALESAAEAGATLANPLGLTNP-----L 57
Db 57 LLVTCIALSAASAPAFLEFFSSQ---KVLNLNQISKSPADRSVAPRLKLDKPEVLLIS 113
QY 63 SLG 65
Db 114 SDG 116

RESULT 7
Q8XW23 PRELIMINARY; PRT; 148 AA.
ID Q8XW23
AC Q8XW23
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable lipoprotein.
GN RSC2652 OR RS04564.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Couzy J., Mangenot S.,
EA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
EA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
EA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502(2002).

Query Match 16.4%; Score 82.5; DB 16; Length 694;
Best Local Similarity 33.3%; Pred. No. 25;
Matches 33; Conservative 11; Mismatches 42; Indels 13; Gaps 4;
QY 3 LAALGLCVALS...AKVPAQVVALESAAEAGATLANPLGLTNP-----L 57
Db 438 MVPLFGISEAMDAGAAFGIWAEPQAPVDV--SAAGAAGG-----GHVTFDEAEA 489
QY 58 KLLLSGIGIPVNHLEIGSKVCVAELGPAQVAVKALKAL 96
Db 490 KARLIKAGLPVKGKAGNAVEAVISSNALGFPVVALKAL 528

RESULT 6
Q9SU83 PRELIMINARY; PRT; 496 AA.
ID Q9SU83
AC Q9SU83
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nucleotide mismatch between the two sequences for 36 nt

Query Match 16.4%; Score 82.5; DB 16; Length 694;
Best Local Similarity 33.3%; Pred. No. 25;
Matches 33; Conservative 11; Mismatches 42; Indels 13; Gaps 4;
QY 3 LAALGLCVALS...AKVPAQVVALESAAEAGATLANPLGLTNP-----L 57
Db 438 MVPLFGISEAMDAGAAFGIWAEPQAPVDV--SAAGAAGG-----GHVTFDEAEA 489
QY 58 KLLLSGIGIPVNHLEIGSKVCVAELGPAQVAVKALKAL 96
Db 490 KARLIKAGLPVKGKAGNAVEAVISSNALGFPVVALKAL 528

RESULT 5
Q98CR1 PRELIMINARY; PRT; 694 AA.
ID Q98CR1
AC Q98CR1
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein mlf5043.
GN Mlf5043.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
EA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti";
RL DNA Res. 7:331-338(2000).

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative invasion protein.
SAV294.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
[1]
SEQUENCE FROM N.A.
RP STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8155;
RC MEDLINE=21477403; PubMed=11572948;
RX Omura S., Ikeda H., Iehikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakai Y., Hattori M.;
RA "genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT

Thu Jun 3 10:25:06 2004

Page 6

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Query Match      15.3%; Score 77; DB 17; Length 453;  
Best Local Similarity 27.8%; Pred. No. 52;  
Matches 30; Conservative 20; Mismatches 34; Indels 24; Gaps 4;  
  
Qy      11 VALSCSAAFLVGSAGKPVAPQVAALSSAABAGAGTIANPLGTINPIK--LLSSLGI--66  
           :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db     102 MAAPAGADVAIIIGSADD-STILDALRSAHKYGVYRVKMADLISAPEIKRAVDLEALGVGYD 160  
           :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
  
Qy      67 -----PYNHLIEGSKCVAEI-----GFOAVGVATKAKA 95  
           ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db     161 INVHVGIDQQMGVRGDPSILMEISKVSQVLAVAGGLDAEGAAKA 208
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RESULT 14

Q8UA14

ID Q8UA14 PRELIMINARY; PRT; 355 AA.

AC Q8UA14;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE ABC transporter, membrane spanning protein.

DE ATU3389 OR AGR L 2865.

GN Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OS Agrobacterium tumefaciens

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

OX NCBI_TaxID=176239;

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=21608550; PubMed=11743193;

RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

RA Chapman F., Clendenning J., Deatherage G., Gillet W., Grant C.,

RA Kutayavon T., Levy R., Li M.-J., McCelland E., Palmieri A.,

RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

RA Nester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens

RT C58. ";

RL Science 294:2317-2323(2001).

RN [2]

SEQUENCE FROM N.A.

RP MEDLINE=21608551; PubMed=11743194;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

RA Houmieg K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,

RA Cielo C., Slater S.;

RT "genome sequence of the plant pathogen and biotechnology agent

RT Agrobacterium tumefaciens C58. ";

RL Science 294:2323-2328(2001).

DR ENBL; AE009269; AAL44202.1; -.

DR EMBL; AE008343; AAK90001.1; -.

DR PIR; AD2973; AD2973.

DR PIR; G98309; G98309.

DR GO; GO:0016020; C:membrane; IEA.

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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:05:19 ; Search time 4.04538 Seconds
(without alignments)
1338.637 Million cell updates/sec

Title: US-09-700-770-9
Perfect score: 502
Sequence: 1 MKLALLGLCVLSCSSAAA.....QAVGAVKALKALGALTVFG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	497	99.0	104	1	UGR2 HUMAN
2	250	49.8	104	1	UGR2 MOUSE
3	160	31.9	93	1	UGR1 HUMAN
4	135	26.9	139	1	UGR1 MOUSE
5	83	16.5	1327	1	TRK1 HUMAN
6	77	15.3	335	1	UGR2 STRCO
7	76	15.1	732	1	COPA HELFE
8	75	14.9	362	1	MDC1 HUMAN
9	75	14.9	362	1	MDC1 MOUSE
10	74	14.7	779	1	SN1L MOUSE
11	73.5	14.6	626	1	DXS WIGHER
12	73.5	14.6	776	1	SN1L RAT
13	73.5	14.6	882	1	SYA THETH
14	72	14.3	397	1	SUCC AGT5
15	71	14.1	428	1	FXB2 MOUSE
16	71	14.1	480	1	DNAH RHIME
17	69	13.7	124	1	RL7 RALSO
18	68.5	13.6	377	1	PROB BIFLO
19	68	13.5	334	1	PEPD ECOLI
20	68	13.5	569	1	SILF MOUSE
21	67.5	13.4	2035	1	Y233 HUMAN
22	67	13.3	331	1	GCP MYCLE
23	67	13.3	464	1	FUMC PSES
24	66.5	13.2	341	1	TA2R RAT
25	66.5	13.2	465	1	FXD1 HUMAN
26	66	13.1	118	1	NLTD BRAOL
27	66	13.1	121	1	NP70 MYCA
28	66	13.1	239	1	CLRC IDEDE
29	66	13.1	527	1	PTB MOUSE
30	66	13.1	540	1	LEUI PROMM
31	66	13.1	585	1	NUPI RAT
32	65.5	13.0	257	1	EUTC RUOER
33	65.5	13.0	336	1	COBI RHILLO

ALIGNMENTS

RESULT :

ID	UGR2 HUMAN	STANDARD;	PRT;	104 AA.
AC	Q96QR1; Q96PL0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobulin family 3A member 1).			
DE	normal-1) (Secretoglobulin family 3A member 1).			
GN	SCGB3A1 OR UGRP2 OR HIN1.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21396515; PubMed=11481438;			
RA	Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P., Kaelin C.M., Rhei E., Rosenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyak K.;			
RA	"HIN-1, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells";			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21539178; PubMed=11682631;			
RA	Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kinura S.;			
RT	"UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";			
RL	Mol. Endocrinol. 15:2021-2036(2001).			
CC	-!- FUNCTION: Potential growth inhibitory cytokine.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in breast cancer cell lines.			
CC	-!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.			
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CC	EMBL; AF040564; AAK82942.1; -			
DR	EMBL; AF313458; AAL26217.1; -			
DR	Genew; HGNC:18384; SCGB3A1.			
DR	MIM; 606500; -			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0005125; P:cytokine activity; NAS.			
DR	GO; GO:0003088; P:negative regulation of cell growth; NAS.			
DR	GO; GO:0042127; P:regulation of cell proliferation; NAS.			
KW	Cytokine; Signal.			
FT	SIGNAL 1 20 POTENTIAL.			

```
FT CHAIN 21 104 UTEROGLOBIN-RELATED PROTEIN 2.
FT CONFLICT 19 R -> A (IN REF. 2).
SQ SEQUENCE 104 AA; 10185 MW; 1083873C8FAE8015 CRC64;

Query Match 99.0%; Score 497; DB 1; Length 104;
Best Local Similarity 99.0%; Pred. No. 7.2e-38;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALSASSAAFLVGSAPVQAQVVALESAAEAGAGTLANPLGTINPLKLL 60
Db 1 MKLAALLGLCVALSASSAAFLVGSAPVQAQVVALESAAEAGAGTLANPLGTINPLKLL 60

QY 61 LSSSLGIPVNHLLIEGSKCVAEIGPOAVGAVKALKALLGALTIVFG 104
Db 61 LSSSLGIPVNHLLIEGSKCVAEIGPOAVGAVKALKALLGALTIVFG 104

RESULT 2
UGR2 MOUSE
ID UGR2 MOUSE STANDARD; PRT; 104 AA.
AC Q92007;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in
DE normal-1) (Secretoglobin family 3A member 1).
GN SCGB3A1 OR UGRP2 OR HIN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2139615; PubMed=11481438;
RA Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,
RA Kaelin C.M., Rhei E., Bosenberg M., Schmitt S., Marks J.R., Pagon Z.,
RA Belina D., Razumovic J., Polyak K.;
RT "HIN-1, a putative cytokine highly expressed in normal but not
RT cancerous mammary epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2139615; PubMed=11481438;
RA Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,
RA Kaelin C.M., Rhei E., Bosenberg M., Schmitt S., Marks J.R., Pagon Z.,
RA Belina D., Razumovic J., Polyak K.;
RT "HIN-1, a putative cytokine highly expressed in normal but not
RT cancerous mammary epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2139178; PubMed=11682631;
RA Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
RA Kimura S.;
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1
RT homeodomain transcription factor.";
RL Mol. Endocrinol. 15:2021-2036(2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
CC -1- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
CC
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CC
CC EMBL; AF313455; AAL26215.1; -.
CC DR EMBL; BC024232; AAL24232.1; -.
CC DR GenBank; U00001.1; -.
CC DR MIM; 606531; -.
CC KW Signal.

Query Match 49.8%; Score 250; DB 1; Length 104;
Best Local Similarity 57.0%; Pred. No. 8.2e-16;
Matches 61; Conservative 14; Mismatches 26; Indels 6; Gaps 4;

QY 1 MKLAALLGLCVALSASSAAFLVGSAPVQAQVVALESAAEAGAGTLANPLGTINPL 57
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DR ProDom; PD001864; Glyco_trans_3; 1.
DR TIGRFAMs; TIGR01245; trpD; 1.
DR Tryptophan biosynthesis; Transferase; Glycosyltransferase;
KW Complete proteome.
SQ SEQUENCE 335 AA; 34536 MW; 2706194E400B2F0D CRC64;

Query Match 15.3%; Score 77; DB 1; Length 335;
Best Local Similarity 34.5%; Pred. No. 6.5;
Matches 30; Conservative 9; Mismatches 36; Indels 12; Gaps 4;

QY 7 LGLCVALSCSAAAFVLSA-----KPAQVAALESAA-----EAGAGTLANPLGTL-NP 56
Db 117 LGVIDLGAERAAACLDRTGTFLEFAPVFP--AFRHTAGPRRELGAFTVFNLLGLPLCNP 174

QY 57 LKLLSSGLGIPVNHILIEGSKQCVBELG 83
Db 175 SGARLTGLGVPSELVEPMTVEVLERLG 201

RESULT 7
COPA_HELPF
ID COPA_HELPF STANDARD; PRT; 732 AA.
AC Q32619;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Copper-transporting ATPase (EC 3.6.3.4).
GN COPA.
OS Helicobacter felis.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49179;
RX MEDLINE=98101471; PubMed=9440521;
RA Bayle D., Waengler S., Weitzneger T., Steinhilber W., Volz J.,
RA Przybylski M., Schaefer K.P., Sachs G., Melchers K.;
RT "Properties of the P-type ATPases encoded by the copA operons of
RT Helicobacter pylori and Helicobacter felis.";
RL J. Bacteriol. 180:317-329 (1998).
CC -!- FUNCTION: PROBABLY INVOLVED IN COPPER EXPORT.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+) (In) = ADP + phosphate +
CC Cu(2+)(Out).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
CC ATPases). Subfamily IB.
CC -!- SIMILARITY: Contains 1 HMA domain.
CC
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CC
CC EMBL; AJ001932; CAA05104.1; -.
CC PIR; T47269; T47269.
CC InterPro; IPR006403; ATPase-IB1_Cu.
CC InterPro; IPR006416; ATPase-IB hvy.
CC InterPro; IPR001757; ATPase_EI-E2.
CC InterPro; IPR001756; Cu ATPase.
CC InterPro; IPR008250; EI-E2 ATPase reg.
CC InterPro; IPR006121; HeavyMe.transpt.
CC InterPro; IPR005834; Hydrolase.
CC InterPro; IPR006191; Metal bind.
CC Pfam; PF00122; EI-E2_ATPase; 1.
CC Pfam; PF00403; HMA; 1.
CC PRINTS; PF00702; Hydrolase; 1.
CC PRINTS; PR00119; CATATPASE.
CC PRINTS; PR00943; CUATPASE.
CC TIGRFAMs; TIGR01511; ATPase-IB1_Cu; 1.

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DR TIGRFAMs; TIGR01525; ATPase-IB hvy; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 3.
DR PROSITE; PS00154; ATPase_E1_E2; 1.
DR PROSITE; PS01047; HMA_1; 1.
DR PROSITE; PS00846; HMA_2; 1.
KW Transport; Ion transport; Copper transport; Hydrolase; ATP-binding;
KW Metal-binding; Copper; Magnesium; Transmembrane; Phosphorylation.
FT DOMAIN 1 88
FT TRANSMEM 89 109
FT DOMAIN 110 122
FT TRANSMEM 123 142
FT DOMAIN 143 149
FT TRANSMEM 150 170
FT DOMAIN 171 187
FT TRANSMEM 188 208
FT DOMAIN 209 336
FT TRANSMEM 337 359
FT DOMAIN 360 365
FT TRANSMEM 366 383
FT DOMAIN 384 663
FT TRANSMEM 664 683
FT DOMAIN 684 694
FT TRANSMEM 695 713
FT DOMAIN 714 732
FT DOMAIN 733 732
FT MOD_RES 421
FT METAL 13 13
FT METAL 16 16
FT METAL 609 609
FT METAL 613 613
SQ SEQUENCE 732 AA; 78853 MW; 7105107EA5949EFD CRC64;

Query Match 15.1%; Score 76; DB 1; Length 732;
Best Local Similarity 26.3%; Pred. No. 16;
Matches 35; Conservative 17; Mismatches 39; Indels 42; Gaps 6;

QY 6 LLGLCVLSCSAAAFVLSAQPVAAL-----ESAAEAGAG----- 45
Db 447 LLTLCASLEAQSEHVIAGKQGIALQEVQVAKPGFGKGVGDQIIKAGNLE 506

QY 46 --TLANPLGTLANPLKLLSS-----LCIPV--NHLIEGSKQVLAELGPQAVGA----- 89
Db 507 FFMPLNPFGLGIGVFGVGTGTLGVVVLADSLKESKEAISEL--KALGVKVTLLSGD 564

QY 90 ----VKALKALIG 98
Db 565 NLENVRALATQLG 577

RESULT 8
MDC1_HUMAN
ID MDC1_HUMAN STANDARD; PRT; 362 AA.
AC Q9H1K6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mesoderm development candidate 1.
GN MESDC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Retina;
RX MEDLINE=21145589; PubMed=11247670;
RA Wines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,
RA Perkins S., Feldman M., McCombie W.R., Holdener B.C.;
RT "Identification of mesoderm development (mesd) candidate genes by
RT comparative mapping and genome sequence analysis.";
RL Genomics 72:88-98 (2001).
CC -!- SIMILARITY: SOME, TO TALIN.
CC

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DR EMBL; AY007810; AAG41058.1; --
DR Genbank; HGNC:13519; MESDC1.
SQ SEQUENCE 362 AA; 37758 MW; 37BF391D663E1D6E CRC64;

Query Match 14.9%; Score 75; DB 1; Length 362;
Best Local Similarity 35.4%; Pred. No. 11;
Matches 28; Conservative 6; Mismatches 33; Indels 12; Gaps 3;

QY 3 LAALGLCVALS-CSSAAAFVGSAPKVAQP-----VAALSAEAGAGT-ANP 50
DB 112 LVELGDLVSLTECSAAAYLAAVATPGAPQGLVDYRVTTCRHEVEQGCAVLRTAP 171
QY 51 LGTLNPLKLLSLGIPVN 69
DB 172 LADMTPLQLLEVSQGLSRN 190

RESULT 9

ID MDC1 MOUSE STANDARD; PRT; 362 AA.
AC Q9ERB8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mesoderm development candidate 1.
GN MESDC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX STRAIN=129/SVJ;
RX MEDLINE=21145589; PubMed=11247670;
RA Wines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,
RA Perkins S., Feldman M., McCombie W.R., Holdener B.C.;
RT "Identification of mesoderm development (mesd) candidate genes by
RT comparative mapping and genome sequence analysis.";
RL Genomics 72:88-98(2001).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Iquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: SOME, TO TALIN.

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DR EMBL; AF311213; AAG33620.1; --
DR EMBL; BC018326; AAH18326.1; --
DR MGD; MGI:1891420; Mesdcl.
SQ SEQUENCE 362 AA; 37786 MW; EFE9BBFC09BB7CBS CRC64;

Query Match 14.9%; Score 75; DB 1; Length 362;
Best Local Similarity 35.4%; Pred. No. 11;
Matches 28; Conservative 6; Mismatches 33; Indels 12; Gaps 3;

QY 3 LAALGLCVALS-CSSAAAFVGSAPKVAQP-----VAALSAEAGAGT-ANP 50
DB 112 LVELGDLVSLTECSAAAYLAAVATPGAPQGLVDYRVTTCRHEVEQGCAVLRTAP 171
QY 51 LGTLNPLKLLSLGIPVN 69
DB 172 LADMTPLQLLEVSQGLSRN 190

RESULT 10

ID SNIL MOUSE STANDARD; PRT; 779 AA.
AC Q60670;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable serine/threonine protein kinase SNF1K (EC 2.7.1.-) (HRT-20)
DE (Myocardial SNF1-like kinase).
GN SNF1K OR MSK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND REVISIONS TO 8; 16-18; 44-45; 316 AND 435.
RX TISSUE=Embryo;
RA Ruiz J.C.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-435 FROM N.A., AND TISSUE SPECIFICITY.
RX TISSUE=Embryo;
RX MEDLINE=95200798; PubMed=7893599;
RA Ruiz J.C., Conlon F.L., Robertson E.J.;
RT "Identification of novel protein kinases expressed in the myocardium
RT of the developing mouse heart.";
RL Mech. Dev. 48:153-164(1994).
CC -!- TISSUE SPECIFICITY: Expressed in lung, skin, ovary, heart and
CC stomach. No expression in brain, liver or skeletal muscle.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -!- SIMILARITY: Contains 1 UBA domain.

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DR EMBL; U11494; AAA67926.2; --
DR HSSP; P24941; 1AQL.
DR MGD; MGI:104754; Snf1lk.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.


```
DR InterPro; IPR001245; Tyr kinase.
DR InterPro; IPR000449; UBA domain.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00300; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278 PROTEIN KINASE.
FT BIND 303 343 UBA.
FT NP BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT SITE 149 149 BY SIMILARITY.
SQ SEQUENCE 779 AA; 85027 MW; 7B08131BC46D9C4E CRC64;

Query Match 14.7%; Score 74; DB 1; Length 779;
Best Local Similarity 32.9%; Pred. No. 26;
Matches 26; Conservative 11; Mismatches 30; Indels 12; Gaps 3;

QY 10 CVALSCSAAALVGSAKFVAQPVAALESAAAGAGTLANP--LGTLPKLLKLLSSLGHP 67
DB 490 CIISSSSATASPSGTSDDLPSAGSEPGAGLGG-LATPGLLTGTSFVRLASPL--- 545
QY 68 VNHLEGGSKQVAELGPOA 86
DB 546 -----GQSATPVLQTOA 558

RESULT 11
DXS_WIGBR
ID DXS_WIGBR STANDARD; PRT; 626 AA.
AC Q8D357;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1-deoxy-D-xylose-5-phosphate synthase (EC 2.2.1.7) (1-
DE deoxyxylose-5-phosphate synthase) (DXP synthase) (DXPS).
GN DXS OR WIGBR1440.
OS Wigglesworthia glossinidia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxID=36870;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; PubMed=12219091;
RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA Aksoy S.;
RT "Genome sequence of the endocellular obligate symbiont of tsetse
RT flies, Wigglesworthia glossinidia.";
RL Nat. Genet. 32:402-407(2002).
CC -!- FUNCTION: Catalyzes the acyloin condensation reaction between C
CC atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield
CC 1-deoxy-D-xylose-5-phosphate (DXP) (By similarity).
CC -!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-
CC deoxy-D-xylose 5-phosphate + CO(2).
CC -!- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By
CC similarity).
CC -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; first step.
CC -!- PATHWAY: Biosynthetic pathway to thiamine and pyridoxol; first
CC step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
CC
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CC EMBL; AB063521; BAC24290.1; -.
DR HAMAP; MF_00315; 1.
DR InterPro; IPR005477; Dxs synth.
DR InterPro; IPR009014; Transketolase C.
DR InterPro; IPR005476; Transketolase C.
DR InterPro; IPR005475; Transketolase CR.
DR InterPro; IPR005474; Transketolase N.
DR Pfam; PF02779; transket_pyr; 1.
DR Pfam; PF02780; transketolase_C; 1.
DR TIGFAMS; TIGR00204; dks; 1.
DR PROSITE; PS00801; TRANSKETOLASE 1; 1.
DR PROSITE; PS00802; TRANSKETOLASE 2; FALSE NEG.
KW Transferase; Flavoprotein; Thiamine pyrophosphate;
KW Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome.
SQ SEQUENCE 626 AA; 69851 MW; C77008D2D82ABE21 CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 626;
Best Local Similarity 30.0%; Pred. No. 24;
Matches 24; Conservative 14; Mismatches 41; Indels 1; Gaps 1;

QY 22 LVGSNAKFAQPVAALESAAAGAGTLANPLGTLPKLLKLLSSLGTPVNHLEGGSKVCV-A 80
DB 546 LIRMAKTHKALITTEENVIMGAGSANNFEIMYKLLVPLNIGIPDNFVSHGSGQTEVRS 605
QY 81 ELGPOAVGAVKALKALLGAL 100
DB 606 SLGLDSIGIKKIKNWLNFL 625

RESULT 12
SNIL_RAT
ID SNIL_RAT STANDARD; PRT; 776 AA.
AC Q9RLU5; Q9R081;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase SNFLK (EC 2.7.1.-) (Salt-
DE inducible protein kinase) (protein kinase KID2).
GN SNFLK OR SIK OR KID2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=99330184; PubMed=10403390;
RA Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.;
RT "Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high
RT salt diet-treated rat adrenal.";
RL FEBS Lett. 453:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M.,
RA Herschman H.R.;
RT "The KID2 gene encodes a protein kinase induced by depolarization in
RT brain.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -!- SIMILARITY: Contains 1 UBA domain.
CC
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CC EMBL; AB020480; BAAG2673.1; -.
DR EMBL; AF106937; AAF14191.1; -.
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DR HSP: P24941; 1A01.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00300; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278 PROTEIN_KINASE.
FT DOMAIN 303 343 UBA.
FT NP_BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
FT CONFLICT 473 473 R -> K (IN REF. 2).
SQ SEQUENCE 776 AA; 84908 MW; 7BF745AF28F17E6E CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 776;
Best Local Similarity 33.7%; Pred. No. 28;
Matches 28; Conservative 11; Mismatches 31; Indels 13; Gaps 4;

QY 10 CVALSCSSAAFLVGSAPVQVPAQVVALESAAEAGAGTLANP--LGTLPKLLKLLSSLGIP 67
DB 490 CLIVSSRAVVSSEGTSSDSCLPFASGEPAGLGG-LATPGLLTGTSFVRLASPFLL--- 545

QY 68 VNHLEGSQKCAELGPQA-VGA 89
DB 546 -----GSGSATPVLQSQAGLGA 562

RESULT 13
SYA_THETH STANDARD; PRT; 882 AA.
AC P74941;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine-tRNA ligase) (Alars).
GN ALAS.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OC NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HB8 / ATCC 27634;
RX MEDLINE=97351141; PubMed=9207019;
RA Lechler A., Martin A., Zuleeg T., Limmer S., Kreutzer R.;
RT "A biologically active 53 kDa fragment of overproduced alanyl-tRNA synthetase from thermus thermophilus HB8 specifically interacts with tRNA ala acceptor helix.";
RL Nucleic Acids Res. 25:2737-2744 (1997).
CC -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl-tRNA(Ala).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC
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CC
CC EMBL; Y08363; CAA69650.1; -.
DR HAMAP; MF_00036; -.
DR InterPro; IPR003156; DHHA1.
DR InterPro; IPR002318; tRNA-synt_2c.

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DR InterPro; IPR006193; tRNA_synt_alaa.
DR Pfam; PF02272; DHHA1; 1.
DR Pfam; PF01411; tRNA-synt_2c; 1.
DR PRINTS; PR00980; TRNASYNTHALA.
DR TIGRFAMs; TIGR00344; alas; 1.
DR PROSITE; PS50860; AA_tRNA_LIGASE_II_ALA; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SQ SEQUENCE 882 AA; 97454 MW; E50E3E34480CFC56 CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 882;
Best Local Similarity 32.6%; Pred. No. 32;
Matches 30; Conservative 12; Mismatches 47; Indels 3; Gaps 2;

QY 6 LLGELCVALSASSAAFLVGSAPVQVPAQVVALESAAEAGAGTLANPLGTLNPKLLKLLSLG 65
DB 681 LCGGCHVVRTGEIGAFILRSEAVSAGVRRIE--AVTGEAIFRFGSLNRLKALAERLE 738

QY 66 IPVNHLEGSQKCAELGPQA-VGA 97
DB 739 VGEAALEERLEKLLAEL-KEXEREVESLKARL 769

RESULT 14
SUCC_AGRU5 STANDARD; PRT; 397 AA.
ID SUCC_AGRU5 STANDARD; PRT; 397 AA.
AC Q8UC60;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Succinyl-CoA synthetase beta chain (EC 6.2.1.5) (SCS-beta).
OS SUCC OR ATU2638 OR AGR_C 4780.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OC NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayvan T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goddard B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Roumel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328 (2001).
CC -!- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA + phosphate.
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: Composed of an alpha chain and a beta chain (By similarity).
CC -!- SIMILARITY: Belongs to the succinate/malate CoA ligase beta subunit family.
CC
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CC EMBL; AE009211; AAL43619.1; -
CC EMBL; AE008177; AAK83359.1; -
CC PIR; AE2900; AE2900.
CC PIR; F97675; F97675.
CC HANAP; MF 00558; -; 1.
CC InterPro; IPR003135; ATP-grasp.
CC InterPro; IPR005809; CoA lig beta.
CC InterPro; IPR005811; CoA ligase.
CC Pfam; PF02222; ATP-grasp; 1.
CC Pfam; PF00549; ligase-CoA; 1.
CC TIGRFAMs; TIGR01016; sucCoABeta; 1.
CC PROSITE; PS01217; SUCCINYL COA LIG 3; FALSE NEG.
KW Ligase; Tricarboxylic acid cycle; Complete proteome.
SQ SEQUENCE 397 AA; 41899 MW; 223CIA3825764F9F CRC64;

Query Match 14.3%; Score 72; DB 1; Length 397;
Best Local Similarity 36.2%; Pred. No. 21;
Matches 29; Conservative 8; Mismatches 31; Indels 12; Gaps 4;

QY 18 AARLVGSAKVQAPVAALAE-SAAEAGAGTIANPLGTLNPLKLLSSLGIPVNHLEGSQ 76
DQ 8 AKALLKGGVAVGVAIVLKVEREAAAKQLPGPLYV---VKSOIHAGG-----RGKG 57
QY 77 KCVAEIQLGQAVGAVKALKAL 96
DQ 58 K-FKELGPDAGGVRLAKSI 76

RESULT 15
FXB2 MOUSE
ID_FXB2_MOUSE STANDARD; PRT; 428 AA.
AC Q64733;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Forkhead box protein B2 (Transcription factor FKX-4).
GN FOXB2 OR FKX4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97014266; PubMed=8861101;
RA Kaestner K.H., Schuetz G., Monaghan A.P.;
RT "Expression of the winged helix genes fkh-4 and fkh-5 defines domains
RT in the central nervous system.";
RL Mech. Dev. 55:221-230(1996).
RN [2]
RP SEQUENCE OF 4-114 FROM N.A.
RC STRAIN=129;
RX MEDLINE=93361500; PubMed=7689224;
RA Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H.,
RA Monaghan A.P., Schuetz G.;
RT "Six members of the mouse forkhead gene family are developmentally
RT regulated.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: Expressed during embryogenesis.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC
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CC -----
CC EMBL; X92591; CAA63335.1; -
CC EMBL; X71942; CAA50744.1; -
CC PIR; D47746; D47746.
CC HSP; Q63245; 2HFH.
CC TRANSFAC; T02442; -
CC MCD; MGI:1347468; Foxb2.
CC InterPro; IPR001766; TF_Fork_head.
CC Pfam; PF00250; Fork_head; 1.
CC PRINTS; PR00053; FORKHEAD.
CC ProDom; PD000425; TF_Fork_head; 1.
CC SMART; SM00339; FH; 1.
CC PROSITE; PS00657; FORK_HEAD_1; 1.
CC PROSITE; PS00658; FORK_HEAD_2; 1.
CC PROSITE; PS00039; FORK_HEAD_3; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
FT DNA_BIND 12 103
FT DOMAIN 139 153 POLY-HIS.
FT DOMAIN 156 162 POLY-HIS.
FT DOMAIN 163 172 POLY-PRO.
FT DOMAIN 217 231 POLY-ALA.
FT DOMAIN 249 258 POLY-ALA.
FT DOMAIN 321 330 POLY-ALA.
FT DOMAIN 396 399 POLY-ALA.
SQ SEQUENCE 428 AA; 45170 MW; DB8A8EFD1E94AB10 CRC64;

Query Match 14.1%; Score 71; DB 1; Length 428;
Best Local Similarity 29.2%; Pred. No. 28;
Matches 33; Conservative 17; Mismatches 43; Indels 20; Gaps 6;

QY 11 VALSCSSAAAFLYGSAKPVQAQ-PVAALSAEAGAGTIANPLGTLNPL-----KL 59
DQ 220 VAAAAAANAAGVSGRLSQFPYPYGLGSAANAASSTGKFPFAIENIIGRDYKG 279
QY 60 LLSSLGIP---VNHL---IEGS-QKCVAEIQLGQAVGAVKALKALKALTYFG 104
DQ 280 VLAQAGGLPLASVMHLCYPPVGLSNVGVSWPH-VGVMDSVAAAAAAG 331

Search completed: June 2, 2004, 20:19:36
Job time : 5.04538 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:14:10 ; Search time 7.07942 Seconds
(without alignments)
1413.099 Million cell updates/sec

Title: US-09-700-770-9
Perfect score: 502
Sequence: 1 MKLAALGLCVLSCSSAAA.....QAVGAVKALKALLGALTVFG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	16.1	496	2 T09931	probable phosphodiesterase I
2	79.5	15.8	1381	2 S60004	hypothetical prote
3	77.5	15.4	601	2 T35054	probable transport
4	77	15.3	335	2 T36304	probable anthranil
5	76	15.1	355	2 AD2973	hypothetical prote
6	76	15.1	355	2 G98309	probable ABC trans
7	76	15.1	699	2 H87275	L-thio-disulfide int
8	76	15.1	732	2 T47269	copper-transportin
9	75.5	15.0	544	2 H72647	hypothetical prote
10	73.5	14.6	331	2 C84358	transport protein
11	73	14.5	502	2 F83553	probable aldehyde
12	73	14.5	584	2 B87315	gamma-glutamyltran
13	73	14.5	1279	2 T13613	hypothetical prote
14	72	14.3	236	2 A52010	amastigote-specifi
15	72	14.3	397	2 AE2900	succinyl-CoA synth
16	72	14.3	397	2 F97675	succinyl-CoA synth
17	72	14.3	528	2 D70968	hypothetical prote
18	71.5	14.2	462	2 B87634	L-serine dehydrata
19	71.5	14.2	874	2 AC3070	ATP-dependent Clp
20	71.5	14.2	887	2 F98216	endopeptidase clp
21	71	14.1	440	2 C83368	probable MPS trans
22	70.5	14.0	668	2 G85160	heat shock protein
23	70.5	14.0	831	2 D71409	probable endopepti
24	70	13.9	431	2 C86178	hypothetical prote
25	70	13.9	452	2 T46147	zinc finger protei
26	70	13.9	477	2 D82179	probable multidrug
27	69.5	13.8	244	2 S75653	hypothetical prote
28	69.5	13.8	396	2 D75454	hypothetical prote
29	69.5	13.8	423	2 C70582	probable PPE prote

30	69.5	13.8	455	2 AD0782	probable L-serine
31	69	13.7	170	2 AF3312	hypothetical prote
32	69	13.7	627	2 D75393	serine proteinase,
33	69	13.7	853	2 T36551	probable ATP-depen
34	69	13.7	3295	2 AB0074	probable adhesin Y
35	68.5	13.6	277	2 F84336	hypothetical prote
36	68.5	13.6	335	2 AB0575	ferric enterobacti
37	68.5	13.6	1724	2 T18343	p-glycoprotein - S
38	68	13.5	334	2 S16296	ferric enterobacti
39	68	13.5	334	2 A85558	ferric enterobacti
40	68	13.5	334	2 E90707	ferric enterobacti
41	67.5	13.4	560	2 F70719	hypothetical prote
42	67.5	13.4	387	2 C75312	branched-chain ami
43	67.5	13.4	1179	2 H82706	hypothetical prote
44	67.5	13.4	1206	2 B87247	probable conserved
45	67.5	13.4	2698	2 B96671	similar to transla

ALIGNMENTS

RESULT 1

T09931
probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T11
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002
C:Accession: T09931
R:Byan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16897
A:Accession: T09931
A:Molecule type: DNA
A:Residues: 1-496 <BEV>
A:Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T1614.190
A:Experimental source: cultivar Columbia; BAC clone T1614
C:Genetics:
A:Gene: ATSP:T1614.190
A:Map position: 4
C:Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4
C:Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase

Query Match	16.1%;	Score 81;	DB 2;	Length 496;
Best Local Similarity	41.3%;	Pred. No. 5.2;		
Matches	26;	Conservative	14;	Mismatches 17;
				Indels 6;
				Gaps 3;
Qy	6	LLGLCVLSCSSAAAFVGSAPVQAQPVAALESAAEAGA--GTLANPLGTLN-PLKLLLS	62	
Db	57	LLVTCIALSAASAFALFFSSQ---KPVLSLNQISKSPAFDRSVARPLKLDKPVLLIS	113	
Qy	63	SLG 65		
Db	114	SDG 116		

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S60004
hypothetical protein - common roundworm retrotransposon R4 (fragment)
C:Species: Ascaris lumbricoides (common roundworm)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Accession: S60004
R:Burke, W.D.; Mueller, F.; Eickbush, T.H.
Nucleic Acids Res. 23, 4628-4634, 1995
A>Title: R4, a non-LTR retrotransposon specific to the large subunit rRNA genes of n
A:Reference number: S60004; MUID:96103592; PMID:8524653
A:Accession: S60004
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1381 <BUR>
A:Cross-references: EMBL:U29445; NID:G903660; PIDN:AAA97394.1; PID:G903661
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C:Genetics:
A:Genome: retrotransposon

RESULT 5

A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2973
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-355 <KUR>
A:Cross-references: GH:AE008699; PIDN:AAU44202.1; PID:gl7741781; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3389
A:Map position: linear chromosome

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	Best Local Similarity	23.3%;	Pred. No. 11;	Mismatches 42;	Indels 28; Gaps 3;
	Matches 28;	Conservative			
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Dd	24 RILIVLGFLALCFMSADMALGPARYLTSEVLA-----TIADPAAVGNQLRVVI	73			
QY	62 SSLGIPIVNHL-----IEGSKCVA-----ELGPQAVGAVKALKALIGALTVF	103			
Dd	74 WDIRMPIALMAYTIVGASLVSAAGAOMOTIISLNPLASPFTLIGISAASFCQAALALVGGAIF	133			

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 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C:Accession: G98309
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goll
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: G98309
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-355 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK90001.1; PID:gl5159970; GSPDB:GN00170
 C:Genetics:
 A:Gene: AGR_L 2865
 A:Map position: linear chromosome

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:19:10 ; Search time 18.5413 Seconds

(without alignments)
1578.054 Million cell updates/sec

Title: US-09-700-770-9

Perfect score:

Sequence: 1 MKLAALLGLCVALSCSSAAA.....QAVGAVKALKALLGALTVEG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

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Minimum DB seq	length: 0
Maximum DB seq	length: 2000000000

Post-processing: Minimum Match 0%

POST-PROCESSING: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	502	100.0	104	9	US-09-989-722-408	Sequence 408, App	
2	502	100.0	104	9	US-09-989-723-408	Sequence 408, App	
3	502	100.0	104	9	US-09-989-729-408	Sequence 408, App	
4	502	100.0	104	9	US-09-989-727-408	Sequence 408, App	
5	502	100.0	104	9	US-09-989-731-408	Sequence 408, App	
6	502	100.0	104	9	US-09-989-732-408	Sequence 408, App	
7	502	100.0	104	9	US-09-991-073-408	Sequence 408, App	
8	502	100.0	104	9	US-08-980-442-408	Sequence 408, App	
9	502	100.0	104	9	US-08-991-163-408	Sequence 408, App	
10	502	100.0	104	9	US-09-993-604-408	Sequence 408, App	
11	502	100.0	104	9	US-09-990-456-408	Sequence 408, App	
12	502	100.0	104	9	US-09-989-721-408	Sequence 408, App	
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14	502	100.0	104	9	US-09-989-293A-408	Sequence 408, App	
15	502	100.0	104	9	US-09-989-735-408	Sequence 408, App	

ALIGNMENTS

RESULT 1

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US-09-989-722-08
; Sequence 408, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secured and Transmembrane Peptide
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIORITY APPLICATION NUMBER: 60/049787
; PRIORITY FILING DATE: 1997-06-16
; PRIORITY APPLICATION NUMBER: 60/062250
; PRIORITY FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 502; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
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Db 1 MKLAALGLCVALSASSAAFLVGSAPVAFVVALESAAAGAGTLANPLGTNLPLKLL 60

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RESULT 2
US-09-989-723-408
; Sequence 408, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gieritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 502; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.5e-47; Indels 0; Gaps 0;
Matches 104; Conservative 0; Mismatches 0;

Qy    1 MKLAALGLCVALS CSSAAFLVGS AKPVAQ PVAALSSAAEAGAGT LANPLGT LNKLL 60
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RESULT 3
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; Sequence 408, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC56
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; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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RESULT 6

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 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC57
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 ; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 7.5e-47; Indels 0; Gaps 0;
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; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Desnoyers, Luc
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Iuc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC25
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 502; DB 9; Length 104;

Best local similarity 100.0%; Pred. No. 7.5e-47; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0;

Qy 1 MKLAALGLCVALSAAFLVNGSAKPVAOPVAALSAAGAGTIANPLGTINPKLL 60

Db 1 MKLAALGLCVALSAAFLVNGSAKPVAOPVAALSAAGAGTIANPLGTINPKLL 60

Qy 61 LSSIGIPVNHLEIGSQKCVAEELGQAVGAVKALKALGALTVEG 104

Db 61 LSSIGIPVNHLEIGSQKCVAEELGQAVGAVKALKALGALTVEG 104

RESULT 12

US-09-989-721-408
 ; Sequence 408, Application US/09989721
 ; Patent No. US20020142961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary B.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zhen
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C55
 ; CURRENT APPLICATION NUMBER: US/09/989,721
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 502; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLAALGLCVALLSCSSAAFLVGSAPVQVPAALLESAAEAGAGTLANPLGTLNPKLL 60
Db 1 MKLAALGLCVALLSCSSAAFLVGSAPVQVPAALLESAAEAGAGTLANPLGTLNPKLL 60

Qy 61 LSSIGIPVNHLEGSQKCVAEELGPQAVGAVKALKALIGALTVEG 104
Db 61 LSSIGIPVNHLEGSQKCVAEELGPQAVGAVKALKALIGALTVEG 104

RESULT 13

US-09-992-598-408
; Sequence 408, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavins, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730FIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04

US-09-989-293A-408
; Sequence 408, Application US/09989293A
; Patent No. US20020177164A1

<p> GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan L. APPLICANT: Ferrara, Napoleone APPLICANT: Fong, Sherman APPLICANT: Gerber, Hanspeter APPLICANT: Gerritsen, Mary E. APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul J. APPLICANT: Grimaldi, J. Christopher APPLICANT: Gurney, Austin L. APPLICANT: Kljavin, Ivar J. APPLICANT: Napier, Mary A. APPLICANT: Pan, James APPLICANT: Paoni, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Watanabe, Colin K. APPLICANT: Williams, P. Mickey APPLICANT: Wood, William I. APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same FILE REFERENCE: P2730PLC66 CURRENT APPLICATION NUMBER: US/09/989,293A CURRENT FILING DATE: 2001-11-20 PRIORITY APPLICATION NUMBER: 60/049787 PRIORITY FILING DATE: 1997-06-16 PRIORITY APPLICATION NUMBER: 60/062250 PRIORITY FILING DATE: 1997-10-17 PRIORITY APPLICATION NUMBER: 60/065186 PRIORITY FILING DATE: 1997-11-12 PRIORITY APPLICATION NUMBER: 60/065311 PRIORITY FILING DATE: 1997-11-13 PRIORITY APPLICATION NUMBER: 60/066770 PRIORITY FILING DATE: 1997-11-24 PRIORITY APPLICATION NUMBER: 60/075945 PRIORITY FILING DATE: 1998-02-25 PRIORITY APPLICATION NUMBER: 60/078910 PRIORITY FILING DATE: 1998-03-20 PRIORITY APPLICATION NUMBER: 60/083322 PRIORITY FILING DATE: 1998-04-28 PRIORITY APPLICATION NUMBER: 60/084600 PRIORITY FILING DATE: 1998-05-07 PRIORITY APPLICATION NUMBER: 60/087106 PRIORITY FILING DATE: 1998-05-28 PRIORITY APPLICATION NUMBER: 60/087607 PRIORITY FILING DATE: 1998-06-02 PRIORITY APPLICATION NUMBER: 60/087609 PRIORITY FILING DATE: 1998-06-02 PRIORITY APPLICATION NUMBER: 60/087759 PRIORITY FILING DATE: 1998-06-02 PRIORITY APPLICATION NUMBER: 60/087827 PRIORITY FILING DATE: 1998-06-03 PRIORITY APPLICATION NUMBER: 60/088021 PRIORITY FILING DATE: 1998-06-04 PRIORITY APPLICATION NUMBER: 60/088025 PRIORITY FILING DATE: 1998-06-04 PRIORITY APPLICATION NUMBER: 60/088026 PRIORITY FILING DATE: 1998-06-04 PRIORITY APPLICATION NUMBER: 60/088028 PRIORITY FILING DATE: 1998-06-04 PRIORITY APPLICATION NUMBER: 60/088029 PRIORITY FILING DATE: 1998-06-04 PRIORITY APPLICATION NUMBER: 60/088030 PRIORITY FILING DATE: 1998-06-04 PRIORITY APPLICATION NUMBER: 60/088033 PRIORITY FILING DATE: 1998-06-04 PRIORITY APPLICATION NUMBER: 60/088326 </p>	<p> PRIOR FILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/088167 PRIOR FILING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60/088202 PRIOR FILING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60/088212 PRIOR FILING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60/088217 PRIOR FILING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60/088655 PRIOR FILING DATE: 1998-06-09 PRIOR APPLICATION NUMBER: 60/088734 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088738 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088742 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088810 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088824 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088826 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088858 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/088861 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/088876 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/089105 PRIOR FILING DATE: 1998-06-12 PRIOR APPLICATION NUMBER: 60/089440 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089512 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089514 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089532 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089538 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089598 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089599 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089600 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089653 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089801 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089907 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089908 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089947 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089948 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089952 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/090246 PRIOR FILING DATE: 1998-06-22 PRIOR APPLICATION NUMBER: 60/090252 PRIOR FILING DATE: 1998-06-22 PRIOR APPLICATION NUMBER: 60/090254 PRIOR FILING DATE: 1998-06-22 PRIOR APPLICATION NUMBER: 60/090349 PRIOR FILING DATE: 1998-06-23 PRIOR APPLICATION NUMBER: 60/090355 PRIOR FILING DATE: 1998-06-23 PRIOR APPLICATION NUMBER: 60/090429 PRIOR FILING DATE: 1998-06-24 </p>
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
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PRIORITY FILING DATE: 1998-06-05

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APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC61
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PRIORITY APPLICATION NUMBER: 60/088167
PRIORITY FILING DATE: 1998-06-05

Query Match 100.0%; Score 502; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALLSCSSAAAFVGSAXPQVPALESAAEAGAGTLANPLGTLNPKLL 60
DB 1 MKLAALLGLCVALLSCSSAAAFVGSAXPQVPALESAAEAGAGTLANPLGTLNPKLL 60
QY 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTIVFG 104
DB 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTIVFG 104

RESULT 15
US-09-989-735-408
Sequence 408, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.

;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
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;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 502; DB 9; Length 104;

Best Local Similarity 100.0%; Pred. No. 7.5e-47;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALSCTSSAAAFVGSAPVQPVAALESAAAGAGTIANPLGTINPLKLL 60

Db 1 MKLAALLGLCVALSCTSSAAAFVGSAPVQPVAALESAAAGAGTIANPLGTINPLKLL 60

QY 61 LSSLGIPVNHLEGSOKCVAEELGPQAVGAVKALKALLGALTVPFG 104

Db 61 LSSLGIPVNHLEGSOKCVAEELGPQAVGAVKALKALLGALTVPFG 104

Search completed: June 2, 2004, 20:25:21

Job time : 20.5413 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:16:40 ; Search time 7.24797 Seconds
(without alignments)
740.773 Million cell updates/sec

Title: US-09-700-770-9
Perfect score: 502
Sequence: 1 MKLAALLGLCVALLSCSSAAA.....QAVGAVKALKALLGALTVEG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	31.9	93	2	US-08-964-725-14
2	83	16.5	673	3	US-09-196-387-8
3	83	16.5	673	4	US-09-841-835-8
4	83	16.5	949	3	US-09-196-387-10
5	83	16.5	949	4	US-09-841-835-10
6	83	16.5	1327	3	US-09-196-387-2
7	83	16.5	1327	4	US-09-841-835-2
8	83	16.5	1327	4	US-09-972-115A-8
9	82.5	16.4	718	4	US-09-252-991A-25696
10	78.5	15.6	255	4	US-09-252-991A-21756
11	77	15.3	540	4	US-09-252-991A-29143
12	73.5	14.6	443	3	US-09-088-425-2
13	73.5	14.6	447	4	US-09-639-378A-2
14	73.5	14.6	776	4	US-09-523-849-34
15	72	14.3	236	1	US-08-452-531-3
16	72	14.3	236	2	US-08-460-746A-3
17	72	14.3	236	2	US-08-460-555-3
18	72	14.3	236	3	US-08-460-666-3
19	69.5	13.8	423	4	US-09-073-009-142
20	69.5	13.8	423	4	US-09-073-010-142
21	69.5	13.8	710	4	US-09-287-849-16
22	69.5	13.8	856	4	US-09-287-849-12
23	69	13.7	468	4	US-09-252-991A-28114
24	68.5	13.6	163	4	US-09-252-991A-22281
25	68	13.5	461	1	US-08-194-338-4
26	68	13.5	480	4	US-09-543-681A-4680
27	67	13.3	419	4	US-09-252-991A-26821

28	66.5	13.2	323	4	US-09-489-039A-13907	Sequence 13907, A
29	66	13.1	310	4	US-09-489-039A-12597	Sequence 12597, A
30	66	13.1	390	4	US-09-647-224A-2	Sequence 2, Appli
31	66	13.1	587	4	US-09-252-991A-31479	Sequence 31479, A
32	66	13.1	638	2	US-08-426-125-4	Sequence 4, Appli
33	66	13.1	638	2	US-08-455-355-4	Sequence 4, Appli
34	66	13.1	638	4	US-09-367-512-3	Sequence 3, Appli
35	66	13.1	1043	4	US-08-851-567B-61	Sequence 61, Appl
36	65.5	13.0	346	4	US-09-134-000C-4469	Sequence 4469, Ap
37	65.5	13.0	407	4	US-09-489-039A-10855	Sequence 10855, A
38	65.5	13.0	593	2	US-08-591-079-8	Sequence 8, Appli
39	65.5	13.0	593	2	US-08-591-079-10	Sequence 10, Appli
40	65.5	13.0	645	4	US-09-543-681A-6140	Sequence 6140, Ap
41	65.5	13.0	4928	3	US-09-036-987A-5	Sequence 5, Appli
42	65.5	13.0	4928	3	US-09-370-700-5	Sequence 5, Appli
43	65.5	13.0	4928	4	US-09-603-207-5	Sequence 5, Appli
44	65	12.9	180	4	US-09-489-039A-12312	Sequence 12312, A
45	65	12.9	269	4	US-09-107-532A-5682	Sequence 5682, Ap

ALIGNMENTS

RESULT 1
US-08-964-725-14
; Sequence 14, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian C.
; APPLICANT: HODGES, Steven C.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear


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RESULT 3
US-09-841-835-8
Sequence 8, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcinin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-841-835-8
Query Match 16.5%; Score 83; DB 4; Length 673;
Best Local Similarity 30.5%; Pred.No. 0.28;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3
QY 15 CSSAAFLVGSAGVAQPVAALSAEA-----EAGAGTLANPLGTLPKLLSSILGIPVN 69
|||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db 90 CSTTCTICVAAAFFV-PAVSTSSGAAGVANPAGSGNNSPSSSSFTSSSSSSPSPCS 148
QY 70 HLIEGSQ----KCVAEIGPQAVGAKALKALLGAL 100
Db 149 SLAESPERAGVSSTAPLGPAGAAGPGTCGPAVSGAL 183

RESULT 4
US-09-196-387-10
Sequence 10, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor

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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-196-387-10

Query Match 16.5%; Score 83; DB 3; Length 949;
Best Local Similarity 30.5%; Pred. No. 0.45;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAFLVGSAPVAPVVALESAA-----EAGAGTLANPLGTLNPKLLSLGIPVN 69
DB 90 CSTTSTICTVAAAPVV-PAVSTSSAAGVAPNPGSGNNSSPSSSTSSSSSSPSSPGS 148
QY 70 HLEIGSQ-----KCVAEIGPQAVGAVKALKALGAL 100
DB 149 SLAESPEAAGVSTAPLPGGAAGPGTGVPVAVSGAL 183

RESULT 5
US-09-841-835-10
Sequence 10, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-841-835-10

Query Match 16.5%; Score 83; DB 4; Length 949;
Best Local Similarity 30.5%; Pred. No. 0.45;
Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSSAAFLVGSAPVAPVVALESAA-----EAGAGTLANPLGTLNPKLLSLGIPVN 69
DB 90 CSTTSTICTVAAAPVV-PAVSTSSAAGVAPNPGSGNNSSPSSSTSSSSSSPSSPGS 148
QY 70 HLEIGSQ-----KCVAEIGPQAVGAVKALKALGAL 100
DB 149 SLAESPEAAGVSTAPLPGGAAGPGTGVPVAVSGAL 183

RESULT 6
US-09-193-387-2
Sequence 2, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Qy 70 HLIQSQ---KCV AELGPQAVGAVKALKALLGAL 100

QY 82 LGPQAVG 88

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Db      198 AGPGLG 204

RESULT 10
US-09-252-991A-21756
; Sequence 21756, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21756
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21756

Query Match      15.6%; Score 78.5; DB 4; Length 255;
Best Local Similarity 24.1%; Pred. No. 0.25; Mismatches 10; Indels 71; Gaps 6;
Matches 39; Conservative 10;

QY      10 CVALSCSSA--AAFLVGSAPVAPVAALESAAEAGA-----GTLANPLGTLNPLK 58
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      59 LLLSLGHPVNH-----LLEG-----LLEG-----74
      65 -LLEGLRVRPHARPEHQVHSGDGTGVLGGLVGGDLGAGLDTFGGQAGLAEHHRQHAEEA 123
      75 -----SOKVAELGPQAVGAV--KALKALLGALTVF 103
      124 GVGADQLFRVGSRCALENGIEAIGVILERAAPFGKGLAVF 165

RESULT 11
US-09-252-991A-29143
; Sequence 29143, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29143
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29143

Query Match      15.3%; Score 77; DB 4; Length 540;
Best Local Similarity 30.0%; Pred. No. 1.1;
Matches 33; Conservative 13; Mismatches 40; Indels 24; Gaps 5;

QY      4 AALLGLCVALSCSSA-----AAFLVGSAPVAPVAALESAAEAGAAGTL 47
      302 AQVLGNLVGSCAAGCAQMAISAAVFVGAAREWIPELAERMAALRPGHQDDAAYGPL 361
      48 ANPLGTLNPLKLLSLGIPVNHIEGSQKCVAE-----LGPQAVGAV 90

Db      198 AGPGLG 204

RESULT 12
US-09-088-425-2
; Sequence 2, Application US/09088425
; Patent No. 6171843
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, OLGA
; APPLICANT: LAL, PREETI
; APPLICANT: CORLEY, NEIL C.
; APPLICANT: PATTERSON, CHANDRA
; APPLICANT: BAUGHN, MARIAH R.
; TITLE OF INVENTION: HUMAN ISOMERASE-LIKE PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,425
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0529 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TMLR3DT01
; CLONE: 289973
US-09-088-425-2

Query Match      14.6%; Score 73.5; DB 3; Length 443;
Best Local Similarity 34.1%; Pred. No. 2.1;
Matches 29; Conservative 9; Mismatches 26; Indels 21; Gaps 4;

QY      35 ALESAAEAGAGTLANPLGTLNPLK-----LLLS-----LGIPVNHIEGSQKCV 79
      326 ALLEALEQG-----QSLGPFVELDGPAGAVLECLVSSGMLVPELAIPVYLL-GALTWL 379
      80 AELGPQAVGAVKALKALLGALTVF 104
      380 SETRAQAAGGGAGVAELLGPLELVG 404

Db      198 AGPGLG 204

RESULT 13
US-09-639-378A-2
; Sequence 2, Application US/09639378A
; Patent No. 6524838
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 19:59:24 ; Search time 24.778 Seconds

(without alignments)
1185.931 Million cell updates/sec

Title: US-09-700-770-9

Perfect score: 502

Sequence: 1 MKLAALLGLCVLSCSSARA.....QAVGAVKALKALIGALTVEG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	100.0	104	3	Aay66757 Membrane-
2	502	100.0	104	3	Aay44458 Human lun
3	502	100.0	104	3	Aay87288 Human sig
4	502	100.0	104	4	Aab65280 Human PRO
5	502	100.0	104	5	Aau86141 Human PRO
6	502	100.0	104	6	Abu58095 Human PRO
7	502	100.0	104	6	Abu59173 Novel hum
8	502	100.0	104	6	Abu82685 Human sec
9	502	100.0	104	6	Aaol19895 Human ute
10	502	100.0	104	6	Abu60604 Human sec
11	502	100.0	104	6	Abul13986 Human PRO
12	502	100.0	104	6	Abu72571 Novel hum
13	502	100.0	104	6	Abu59320 Human sec
14	502	100.0	104	6	Abu26017 Human PRO
15	502	100.0	104	6	Abu59026 Human sec
16	502	100.0	104	6	Abu92404 Novel hum
17	502	100.0	104	6	Abu59469 Novel hum
18	502	100.0	104	6	Abu92235 Novel hum
19	502	100.0	104	6	Abu10941 Human PRO
20	502	100.0	104	6	Abu81693 Novel hum
21	502	100.0	104	6	Abu88632 Human sec
22	502	100.0	104	6	Abu34146 Human PRO
23	502	100.0	104	6	Ada37919 Human sec
24	502	100.0	104	6	Ada21605 Human sec
25	502	100.0	104	6	Ada10392 Human sec

ALIGNMENTS

RESULT 1

AAY66757

ID AAY66757 standard; protein; 104 AA.

AC AAY66757;

XX 05-JUN-2000 (first entry)

DT Membrane-bound protein PRO1245.

DB Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

XX Membrane-bound polypeptide; receptor immunoadhesin; gene mapping.

KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX Homoc sapiens.

XX W09963088-A2.

XX 09-DEC-1999.

PF 02-JUN-1999; 99WO-US012252.

XX 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 03-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088722P.

PR 10-JUN-1998; 98US-0088730P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088741P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.

Ada17936 Human PRO
Ada28044 Human sec
Ada94624 Human sec
Ada38849 Human sec
Ada92970 Human sec
Abo53232 Human sec
Ada22531 Human sec
Abo22602 Human sec
Ada06697 Human sec
Ada39390 Human sec
Adb96416 Human PRO
Adb57888 Human PRO
Adb55252 Human PRO
Adci12119 Human PRO
Adci56541 Human PRO
Adci07596 Human sec
Adci1586 Human sec
Adci14708 Novel hum
Add08240 Novel hum
Adc82065 Human PRO

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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 11-JUN-1998; 98US-0089000P.
PR 12-JUN-1998; 98US-0089105P.
PR 12-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089807P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
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PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.

PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
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PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wool WI, Yuan J;
XX WPI; 2000-072883/06.
XX N-PSDB; AAZ65103.
XX Membrane-bound proteins and related nucleotide sequences.
XX Claim 12; Fig 290; 822pp; English.
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
XX Sequence 104 AA;
XX
XX Query Match 100.0%; Score 502; DB 3; Length 104;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-48;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGCVLSCSSAAAFVLSAKPVAQPVAALESAAEAGAGTIANPLGTINPKLL 60
DB 1 MKLAALLGCVLSCSSAAAFVLSAKPVAQPVAALESAAEAGAGTIANPLGTINPKLL 60
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QY 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104
DB 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104

RESULT 2
AAAY44458
ID AAY44458 standard; protein; 104 AA.

XX AC AAY44458;
XX DT 27-MAR-2000 (first entry)
XX DE Human lung specific gene protein Lng107.
XX KW Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate;
XX KW lung cancer; diagnosis.
XX OS Homo sapiens.
XX EN WO960160-AL.
XX PD 25-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010344.
XX PR 21-MAY-1998; 98US-0086212P.
XX PA (DIAD-) DIADEXUS LLC.
XX PI Yang F, Macina RA, Sun Y;
XX WPI; 2000-116320/10.
XX DR N-PSDB; AAZ29723.
XX PT A new method for diagnosing, monitoring and staging lung cancer.
XX PS Example 2; Page 38-39; 40pp; English.

CC The present sequence is a lung specific gene (LSG) protein Lng107 from
CC human clone ID 586271. The LSG has high level of tissue specificity for
CC lungs and is overexpressed in cancerous tissues. The sequence serves as a
CC diagnostic marker for detecting, monitoring, staging and prognosticating
CC lung cancer. The diagnosis involves comparing levels of LSG in samples
CC obtained from patient and normal control
XX SQ Sequence 104 AA;
Query Match 100.0%; Score 502; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALLGLCVLSCSSAAAFVLSGAKPVAQPVALESAAEAGAGTIANPLGTLNPKLL 60
DB 1 MKLAALLGLCVLSCSSAAAFVLSGAKPVAQPVALESAAEAGAGTIANPLGTLNPKLL 60
QY 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104
DB 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104

RESULT 3
AAAY87288
ID AAY87288 standard; protein; 104 AA.
XX AC AAY87288;
XX DT 11-MAY-2000 (first entry)
XX DE Human signal peptide containing protein HSPP-65 SEQ ID NO:65.
XX KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
KW muscular dystrophy.

XX OS Homo sapiens.
XX PN WO200000610-A2.
XX PD 06-JAN-2000.
XX PF 25-JUN-1999; 99WO-US014484.
XX PR 26-JUN-1998; 98US-0090762P.
XX PR 31-JUL-1998; 98US-0094983P.
XX PR 01-OCT-1998; 98US-0102686P.
XX PR 11-DEC-1998; 98US-0112129P.
XX PA (INCY-) INCYTE PHARM INC.

XX PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn ME;
XX PI Akertlom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
XX PI Bandman O;
XX WPI; 2000-160673/14.
XX DR N-PSDB; AAZ98173.

XX PT New human signal peptide-containing proteins useful in treatment,
XX PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
XX PT disease.
XX PS Claim 1; Page 206; 327pp; English.

XX CC AAZ98109 to AAZ98242 encode AAY87357 which represent the
XX CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
XX CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, be
XX CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
XX CC used in gene therapy. HSPPs can be used to treat or prevent disorders
XX CC associated with decreased activity or function of HSPP. Antagonists of
XX CC HSPP are used to treat or prevent disorders associated with increased
XX CC activity or function of HSPP. Such diseases include cell proliferation
XX CC (including cancer), inflammation, cardiovascular, neurological,
XX CC reproductive or developmental disorders, (e.g. arteriosclerosis,
XX CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX CC asthma, Crohn's disease, microbial or other infections, congestive or
XX CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
XX CC nucleic acids can be used for the recombinant production of HSPP, for
XX CC detecting HSPP in standard hybridisation and amplification assays (for
XX CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
XX CC or ribozyme therapeutics, for detecting related sequences or genetic
XX CC variations, and for chromosomal mapping. HSPP are also used to raise
XX CC specific antibodies (Ab) and to screen for agonists and antagonists
XX CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP
XX CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
XX CC competitive drug screens, and for purification of HSPP from natural
XX CC sources

XX SQ Sequence 104 AA;

Query Match 100.0%; Score 502; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVLSCSSAAAFVLSGAKPVAQPVALESAAEAGAGTIANPLGTLNPKLL 60
DB 1 MKLAALLGLCVLSCSSAAAFVLSGAKPVAQPVALESAAEAGAGTIANPLGTLNPKLL 60
QY 61 LSSLGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104

chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

Query Match 100.0%; Score 502; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48; Indels 0; Gaps 0;
Matches 104; Conservative 0; Mismatches 0;
QY 1 MKLAALLGLCVLSCSSAAAFVGSAPVQAPVAALESAAEAGAGTLANPLGTLNPKLL 60
Db 1 MKLAALLGLCVLSCSSAAAFVGSAPVQAPVAALESAAEAGAGTLANPLGTLNPKLL 60
QY 61 LSSLGIPVNHLEIGSKCVAEFGPQAVGAVKALKALGALTVEG 104
Db 61 LSSLGIPVNHLEIGSKCVAEFGPQAVGAVKALKALGALTVEG 104

RESULT 5
AAU86141
ID AAU86141 standard; protein; 104 AA.
XX AC AAU86141;
XX DT 15-JUL-2002 (first entry)
XX DE Human PRO1245 polypeptide.
XX KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
KW neuroprotective.
XX OS Homo sapiens.
XX PN WO20153486-A1.
XX PD 26-JUL-2001.
XX PF 11-FEB-2000; 2000WO-US003565.
XX PR 08-MAR-1999; 99WO-US005028.
PR 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Goddard A, Godowski RJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX WF; 2002-205567/26.

CC chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

Query Match 100.0%; Score 502; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48; Indels 0; Gaps 0;
Matches 104; Conservative 0; Mismatches 0;
QY 1 MKLAALLGLCVLSCSSAAAFVGSAPVQAPVAALESAAEAGAGTLANPLGTLNPKLL 60
Db 1 MKLAALLGLCVLSCSSAAAFVGSAPVQAPVAALESAAEAGAGTLANPLGTLNPKLL 60
QY 61 LSSLGIPVNHLEIGSKCVAEFGPQAVGAVKALKALGALTVEG 104
Db 61 LSSLGIPVNHLEIGSKCVAEFGPQAVGAVKALKALGALTVEG 104

RESULT 5
AAU86141
ID AAU86141 standard; protein; 104 AA.
XX AC AAU86141;
XX DT 15-JUL-2002 (first entry)
XX DE Human PRO1245 polypeptide.
XX KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
KW neuroprotective.
XX OS Homo sapiens.
XX PN WO20153486-A1.
XX PD 26-JUL-2001.
XX PF 11-FEB-2000; 2000WO-US003565.
XX PR 08-MAR-1999; 99WO-US005028.
PR 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Goddard A, Godowski RJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX WF; 2002-205567/26.

DR N-PSDB; ABK40267.
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
XX Claim 61; Fig 28; 302pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumors (e.g. renal, kidney, bladder,
CC breast, etc), leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC stromal and blastocoeleic disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention.
XX
XX Sequence 104 AA;
SQ
Query Match 100.0%; Score 502; DB 5; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALGLCVLSCSAAAFVLGSAKFPVAALESAAEAGAGTLANPLGTLNPLKLL 60
Db 1 MKLAALGLCVLSCSAAAFVLGSAKFPVAALESAAEAGAGTLANPLGTLNPLKLL 60
QY 61 LSSGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104
Db 61 LSSGIPVNHLEGSQKVAELGPOAVGAVKALKALLGALTVEG 104
RESULT 6
ABUS8095
ID ABUS8095 standard; protein; 104 AA.
XX
AC ABUS8095;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #127.
XX
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
XX US2003027163-A1.
XX
PD 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088026P.
104-JUN-1998; 98US-0088028P.
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98US-0088033P.
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98US-0091646P.
98US-0091673P.
98US-0091978P.
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98US-0092182P.
98US-0092472P.
98US-0093339P.
98US-0094651P.

Accession	Date	Score	DB	Length	Indels	Gaps
02-MAR-2000	2000WO-US005841					
10-MAR-2000	2000WO-US006319					
15-MAR-2000	2000WO-US006884					
20-MAR-2000	2000WO-US007377					
30-MAR-2000	2000WO-US008439					
15-MAY-2000	2000WO-US013358					
17-MAY-2000	2000WO-US013705					
22-MAY-2000	2000WO-US014042					
30-MAY-2000	2000WO-US014941					
02-JUN-2000	2000WO-US015264					
23-JUN-2000	2000US-0213637P					
28-JUL-2000	2000WO-US020710					
11-AUG-2000	2000WO-US022031					
23-AUG-2000	2000WO-US023522					
24-AUG-2000	2000WO-US023328					
07-SEP-2000	2000US-0230978P					

Query Match .100.0%; Score 502; DB 6; Length 104;

Best Local Similarity 100.0%; Pred. No. 1.4e-48;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Accession	Date	Score	DB	Length	Indels	Gaps
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04-AUG-1998	98US-0095285P					
04-AUG-1998	98US-0095301P					
04-AUG-1998	98US-0095302P					
04-AUG-1998	98US-0095318P					
04-AUG-1998	98US-0095321P					
04-AUG-1998	98US-0095325P					
10-AUG-1998	98US-0095916P					
10-AUG-1998	98US-0095929P					
10-AUG-1998	98US-0096012P					
11-AUG-1998	98US-0096143P					
11-AUG-1998	98US-0096146P					
12-AUG-1998	98US-0096329P					
17-AUG-1998	98US-0096757P					
17-AUG-1998	98US-0096766P					
17-AUG-1998	98US-0096768P					
17-AUG-1998	98US-0096773P					
17-AUG-1998	98US-0096791P					
17-AUG-1998	98US-0096867P					
17-AUG-1998	98US-0096891P					
17-AUG-1998	98US-0096894P					
17-AUG-1998	98US-0096895P					
17-AUG-1998	98US-0096897P					
18-AUG-1998	98US-0096949P					
18-AUG-1998	98US-0096950P					
18-AUG-1998	98US-0096959P					
18-AUG-1998	98US-0096960P					
18-AUG-1998	98US-0097022P					
19-AUG-1998	98US-0097141P					
20-AUG-1998	98US-0097218P					
24-AUG-1998	98US-0097661P					
26-AUG-1998	98US-0097952P					
26-AUG-1998	98US-0097954P					
26-AUG-1998	98US-0097955P					
26-AUG-1998	98US-0097971P					
26-AUG-1998	98US-0097974P					
26-AUG-1998	98US-0097978P					
26-AUG-1998	98US-0097979P					
26-AUG-1998	98US-0097986P					
26-AUG-1998	98US-0098014P					
31-AUG-1998	98US-0098525P					
16-SEP-1998	98US-0100634P					
16-SEP-1998	98WO-US019330					
17-SEP-1998	98US-0100858P					
17-SEP-1998	98WO-US019437					
07-OCT-1998	98WO-US021141					
01-DEC-1998	98WO-US025108					
22-DEC-1998	98US-0113296P					
05-JAN-1999	99WO-US000106					
08-MAR-1999	99WO-US005028					
12-MAR-1999	99US-0123957P					
02-JUN-1999	99WO-US012252					
23-JUN-1999	99US-0141037P				</	

XX	ABU82685;	PR	19-JUN-1998;	98US-0089948P.
AC		PR	19-JUN-1998;	98US-0089952P.
XX		PR	22-JUN-1998;	98US-0090246P.
DT		PR	22-JUN-1998;	98US-0090252P.
XX	26-JUN-2003 (first entry)	PR	22-JUN-1998;	98US-0090254P.
DE	Human secreted/transmembrane protein PR01245.	PR	23-JUN-1998;	98US-0090349P.
XX		PR	23-JUN-1998;	98US-0090355P.
KW	Human; PRO; secreted protein; transmembrane protein; wound healing;	PR	24-JUN-1998;	98US-0090429P.
KW	cardiac insufficiency disorders; angiogenesis; wound healing;	PR	24-JUN-1998;	98US-0090431P.
KW	cancerous tumour; immune response; retinal disorder; sight loss;	PR	24-JUN-1998;	98US-0090435P.
KW	retinitis pigmentosum; age-related macular degeneration; AMD;	PR	24-JUN-1998;	98US-0090444P.
KW	kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;	PR	24-JUN-1998;	98US-0090445P.
KW	Crohn's disease; sports injury; arthritis.	PR	24-JUN-1998;	98US-0090472P.
XX		PR	24-JUN-1998;	98US-0090535P.
OS	Homo sapiens.	PR	24-JUN-1998;	98US-0090540P.
XX		PR	24-JUN-1998;	98US-0090542P.
XX		PR	24-JUN-1998;	98US-0090557P.
PN	US2003032023-A1.	PR	25-JUN-1998;	98US-0090676P.
XX		PR	25-JUN-1998;	98US-0090678P.
PD	13-FEB-2003.	PR	25-JUN-1998;	98US-0090690P.
XX		PR	25-JUN-1998;	98US-0090694P.
PF	14-NOV-2001; 2001US-00990711.	PR	25-JUN-1998;	98US-0090695P.
XX		PR	25-JUN-1998;	98US-0090696P.
PR	16-JUN-1997;	PR	26-JUN-1998;	98US-0090862P.
PR	17-OCT-1997;	PR	26-JUN-1998;	98US-0090863P.
PR	05-NOV-1997;	PR	01-JUL-1998;	98US-0091360P.
PR	12-NOV-1997;	PR	01-JUL-1998;	98US-0091360P.
PR	13-NOV-1997;	PR	02-JUL-1998;	98US-0091544P.
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PR	20-MAR-1998;	PR	02-JUL-1998;	98US-0091626P.
PR	28-APR-1998;	PR	02-JUL-1998;	98US-0091628P.
PR	07-MAY-1998;	PR	02-JUL-1998;	98US-0091633P.
PR	28-MAY-1998;	PR	02-JUL-1998;	98US-0091646P.
PR	02-JUN-1998;	PR	02-JUL-1998;	98US-0091673P.
PR	02-JUN-1998;	PR	07-JUL-1998;	98US-0091978P.
PR	03-JUN-1998;	PR	07-JUL-1998;	98US-0091982P.
PR	04-JUN-1998;	PR	09-JUL-1998;	98US-0092182P.
PR	04-JUN-1998;	PR	10-JUL-1998;	98US-0092472P.
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PR	04-JUN-1998;	PR	30-JUL-1998;	98US-0094651P.
PR	04-JUN-1998;	PR	04-AUG-1998;	98US-0095282P.
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PR	04-JUN-1998;	PR	04-AUG-1998;	98US-0095302P.
PR	04-JUN-1998;	PR	04-AUG-1998;	98US-0095318P.
PR	04-JUN-1998;	PR	04-AUG-1998;	98US-0095321P.
PR	04-JUN-1998;	PR	04-AUG-1998;	98US-0095325P.
PR	04-JUN-1998;	PR	10-AUG-1998;	98US-0095916P.
PR	04-JUN-1998;	PR	10-AUG-1998;	98US-0095929P.
PR	04-JUN-1998;	PR	10-AUG-1998;	98US-0096012P.
PR	04-JUN-1998;	PR	11-AUG-1998;	98US-0096143P.
PR	04-JUN-1998;	PR	11-AUG-1998;	98US-0096146P.
PR	04-JUN-1998;	PR	12-AUG-1998;	98US-0096329P.
PR	04-JUN-1998;	PR	17-AUG-1998;	98US-0096757P.
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PR	04-JUN-1998;	PR	18-AUG-1998;	98US-0096960P.
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PR	04-JUN-1998;	PR	19-AUG-1998;	98US-0097141P.
PR	04-JUN-1998;	PR	19-AUG-1998;	98US-0097218P.
PR	04-JUN-1998;	PR	20-AUG-1998;	98US-0097661P.
PR	04-JUN-1998;	PR	26-AUG-1998;	98US-0097952P.
PR	04-JUN-1998;	PR	26-AUG-1998;	98US-0097954P.

DT 11-AUG-2003 (first entry)
XX Human uteroglobin related protein 2.
DE UGRP1; human; mouse; promoter; uteroglobin related protein 1;
XX respiratory disorder; asthma.
KW Homo sapiens.
OS WO2003000111-A2.
XX 03-JAN-2003.
PD 18-JUN-2002; 2002WO-US019456.
XX 20-JUN-2001; 2001US-0299828P.
XX (US\$H) US DEPT HEALTH & HUMAN SERVICES.
XX Kimura S, Niimi T;
XX WPI; 2003-184004/18.
XX New human UGRP1 nucleic acid, useful for diagnosing or predicting a
PT predisposition to develop a respiratory disorder or determining the
PT prognosis of a subject having or suspected of having a respiratory
PT disorder e.g., asthma.
XX Disclosure; Page 79-80; 83pp; English.
XX The present invention provides the human and murine uteroglobin related
CC protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis
CC of and prediction of predisposition to respiratory disorders such as
CC asthma. The present sequence is a protein sequence shown in the
CC exemplification of the invention
XX Sequence 104 AA;
SQ
Query Match 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALLGLCVALLSCSSAAAFVGSAPVAPVAALESAAEAGAGTLANPLGTINPLKLL 60
DB 1 MKLAALLGLCVALLSCSSAAAFVGSAPVAPVAALESAAEAGAGTLANPLGTINPLKLL 60
QY 61 LSSLGIPVNHLEIGSKVVAELGPOAVGAVKALKALLGALTIVFG 104
DB 61 LSSLGIPVNHLEIGSKVVAELGPOAVGAVKALKALLGALTIVFG 104
RESULT 1)
ABU50604 standard; protein; 104 AA.
XX
AC ABU50604;
XX
DT 01-MAY-2003 (first entry)
XX Human secreted/transmembrane protein, #163.
DE Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; therapeutic; gene therapy.
XX Homo sapiens.
OS US2002160384-A1.
XX 31-OCT-2002.
PD 14-NOV-2001; 2001US-00992598.
XX 16-JUN-1997; 97US-0049787P.
PR

PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
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PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98US-0101933P.
PR 17-SEP-1998; 98US-0100858P.
PR 07-OCT-1998; 98US-0102114P.
PR 01-DEC-1998; 98US-0102510P.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99US-0144758P.
PR 08-MAR-1999; 99US-0123957P.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99US-0141037P.
PR 23-JUN-1999; 99US-0143048P.
PR 07-JUL-1999; 99US-0144758P.
PR 20-JUL-1999; 99US-0145698P.
PR 26-JUL-1999; 99US-0146222P.
PR 28-JUL-1999; 99US-0149396P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99US-0149396P.
PR 15-SEP-1999; 99US-0149396P.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99US-028313P.
PR 01-DEC-1999; 99US-028313P.
PR 01-DEC-1999; 99US-028634P.
PR 16-DEC-1999; 99US-030095P.
PR 20-DEC-1999; 99US-030095P.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
Query Match 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALLGLCVALLSCSSAAAFVGSAPVAPVAALESAAEAGAGTLANPLGTINPLKLL 60
DB 1 MKLAALLGLCVALLSCSSAAAFVGSAPVAPVAALESAAEAGAGTLANPLGTINPLKLL 60
QY 61 LSSLGIPVNHLEIGSKVVAELGPOAVGAVKALKALLGALTIVFG 104
DB 61 LSSLGIPVNHLEIGSKVVAELGPOAVGAVKALKALLGALTIVFG 104
RESULT 9
AAO19895
ID AAO19895 standard; protein; 104 AA.
XX
AC AAO19895;
XX

17-OCT-1997;	PR	97US-0062250P;
05-NOV-1997;	PR	97WO-US002006P;
12-NOV-1997;	PR	97US-0065186P;
13-NOV-1997;	PR	97US-0065311P;
24-NOV-1997;	PR	97US-0066770P;
25-FEB-1998;	PR	98US-0075945P;
20-MAR-1998;	PR	98US-0078910P;
28-APR-1998;	PR	98US-0083322P;
07-MAY-1998;	PR	98US-0084600P;
28-MAY-1998;	PR	98US-0087106P;
02-JUN-1998;	PR	98US-0087607P;
02-JUN-1998;	PR	98US-0087609P;
02-JUN-1998;	PR	98US-0087759P;
03-JUN-1998;	PR	98US-0087827P;
04-JUN-1998;	PR	98US-0088021P;
04-JUN-1998;	PR	98US-0088025P;
04-JUN-1998;	PR	98US-0088026P;
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09-JUN-1998;	PR	98US-0088655P;
10-JUN-1998;	PR	98US-0088734P;
10-JUN-1998;	PR	98US-0088738P;
10-JUN-1998;	PR	98US-0088742P;
10-JUN-1998;	PR	98US-0088810P;
10-JUN-1998;	PR	98US-0088824P;
11-JUN-1998;	PR	98US-0088826P;
11-JUN-1998;	PR	98US-0088858P;
11-JUN-1998;	PR	98US-0088862P;
12-JUN-1998;	PR	98US-0088876P;
12-JUN-1998;	PR	98US-0089105P;
16-JUN-1998;	PR	98US-0089440P;
16-JUN-1998;	PR	98US-0089512P;
16-JUN-1998;	PR	98US-0089514P;
17-JUN-1998;	PR	98US-0089532P;
17-JUN-1998;	PR	98US-0089538P;
17-JUN-1998;	PR	98US-0089598P;
17-JUN-1998;	PR	98US-0089599P;
17-JUN-1998;	PR	98US-0089600P;
18-JUN-1998;	PR	98US-0089653P;
18-JUN-1998;	PR	98US-0089601P;
18-JUN-1998;	PR	98US-0089907P;
18-JUN-1998;	PR	98US-0089908P;
16-SEP-1998;	PR	98WO-US019330;
7-SEP-1998;	PR	98WO-US019437;
07-OCT-1998;	PR	98WO-US021141;
01-DEC-1998;	PR	98WO-US025108;
01-DEC-1999;	PR	99WO-US000106;
08-MAR-1999;	PR	99WO-US005028;
02-JUN-1999;	PR	99WO-US012252;
15-SEP-1999;	PR	99WO-US012090;
15-SEP-1999;	PR	99WO-US021547;
30-NOV-1999;	PR	99WO-US028313;
01-DEC-1999;	PR	99WO-US028301;
16-DEC-1999;	PR	99WO-US028634;
20-DEC-1999;	PR	99WO-US030095;
05-JAN-2000;	PR	99WO-US030911;
06-JAN-2000;	PR	2000WO-US000219;
11-FEB-2000;	PR	2000WO-US000376;
18-FEB-2000;	PR	2000WO-US003565;
22-FEB-2000;	PR	2000WO-US004341;
24-FEB-2000;	PR	2000WO-US004414;
24-FEB-2000;	PR	2000WO-US004914;
02-MAR-2000;	PR	2000WO-US005004;
11-MAR-2000;	PR	2000WO-US005841;
15-MAR-2000;	PR	2000WO-US006619;
15-MAR-2000;	PR	2000WO-US006884;

XX AC ABU13986;
 XX DT 26-FEB-2003 (first entry)
 XX DE Human PRO1245 polypeptide.
 XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;
 KW genetic disorder; antibacterial; immunosuppressive.
 XX OS Homo sapiens.
 XX PN US2002103125-A1.
 XX DD 01-AUG-2002.
 XX PF 20-NOV-2001; 2001US-00989731.
 XX PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0085186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
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 PR 09-JUN-1998; 98US-0088653P.
 PR 10-JUN-1998; 98US-0088734P.
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 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
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 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 16-DEC-1999; 99WO-US030095.
 PR 06-DEC-1999; 99WO-US030911.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US0003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019892.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 XX (GUTH) GENENTECH LTD.
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood MT;
 PI Zhang Z;
 XX WPI; 2003-102117/09.
 DR N-P3DB; ABX64209.
 XX Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX Claim 12; Fig 290; 649pp; English.
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The polynucleotide sequences
 CC encoding PRO polypeptides are useful as hybridisation probes, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC in the preparation of PRO polypeptides, for generating transgenic animals
 CC or knockout animals, to construct hybridisation probes for mapping the
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome markers, and for generating probes for PCR,
 CC Northern analysis, Southern analysis and Western analysis. ABU13860-
 CC ABU14006 represent the human PRO polypeptides of the invention. Note: The
 CC sequence data for this patent was obtained in electronic format directly

Thu Jun 3 10:25:05 2004

us-09-700-770-9.rag

CC from the USPTO web site at seqdata.uspto.gov/psipsdIDEntry.html

XX SQ Sequence 104 AA;

Query Match 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALSCTSSAAFLVGSAPVQPVAALESAAAGAGTLANPLGTINPLKLL 60
DB 1 MKLAALLGLCVALSCTSSAAFLVGSAPVQPVAALESAAAGAGTLANPLGTINPLKLL 60

QY 61 LSSGIPVNHLEIGSKQVAGLGPQAVGAVKALKALLGALTTFVG 104

DB 61 LSSGIPVNHLEIGSKQVAGLGPQAVGAVKALKALLGALTTFVG 104

RESULT 12

ABU72571

ID ABU72571 standard; protein; 104 AA.

XX AC ABU72571;

XX DT 17-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO1245.

XX KW Human; secreted and transmembrane protein; cytosolic; anti-HIV;
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioindicator; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening.

XX OS Homo sapiens.

XX PN US2003003531-A1.

XX PD 02-JAN-2003.

XX PF 19-NOV-2001; 2001US-00989734.

XX PR 16-JUN-1997; 97US-0049787P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 05-NOV-1997; 97WO-US020069.

XX PR 12-NOV-1997; 97US-0065186P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 24-NOV-1997; 97US-0066770P.

XX PR 25-FEB-1998; 98US-0075945P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 28-APR-1998; 98US-0083332P.

XX PR 07-MAY-1998; 98US-0084600P.

XX PR 28-MAY-1998; 98US-0087106P.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 02-JUN-1998; 98US-0087759P.

XX PR 03-JUN-1998; 98US-0087827P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088026P.

XX PR 04-JUN-1998; 98US-0088028P.

XX PR 04-JUN-1998; 98US-0088029P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 04-JUN-1998; 98US-0088033P.

XX PR 05-JUN-1998; 98US-0088326P.

XX PR 05-JUN-1998; 98US-0088167P.

XX PR 05-JUN-1998; 98US-0088202P.

XX PR 05-JUN-1998; 98US-0088212P.

XX PR 05-JUN-1998; 98US-0088217P.

XX PR 09-JUN-1998; 98US-0088655P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088738P.

XX PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 16-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein D, Deanoyers L, Eaton DL;
XX PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
XX PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX PI Zhang Z;

XX WFI; 2003-352829/33.
DR N-PSDB; ACA64431.
DR

XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
XX
PS Claim 12; Fig 290; 663pp; English.
XX
XX The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide
XX
XX Sequence 104 AA;
SQ

Query Match 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLAALLGLCVALLSCSSAAFLVGSAPVAPVAALESAAEAGAGTLANPIGLTNPKLL 60
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Qy 61 LSSGIPVNHILEGSKVCAELGPOAVGAVKALKALLGALTIVFG 104
Db 61 LSSGIPVNHILEGSKVCAELGPOAVGAVKALKALLGALTIVFG 104

RESULT 13
ABU59320
ID ABU59320 standard; protein; 104 AA.
XX
AC ABU59320;
XX
DT 22-APR-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #163.
XX
XX Human; PRO; secreted; transmembrane; pharmaceutical; diagnostic;
KW biosensor; bioreactor; tumour; therapeutic; gene therapy;
KW tumour-associated antigenic target; TAT; ADSEPT;
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.
XX
XX Homo sapiens.
XX
XX US2003027162-A1.
PN
XX
PD 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997428.
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XX 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.

28-APR-1998; 98US-0083322P.
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PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
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PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
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PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089633P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021030.
PR 15-SEP-1999; 99WO-US021547.
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PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005044.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PI Geribaldi JC, Gurney AL, Kijavini J, Napier MA, Pan J, Paoni NF;
PI Roy WA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2003-340824/32.
DR N-PEDB; ACD44399.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT and are therapeutically useful for enhancing immune responses.
XX
PS Claim 12; Fig 290; 661pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for-
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. ABO25891-
CC ABO26037 represent the human PRO polypeptides of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipdbidentry.html
XX
SQ Sequence 104 AA;
Query Match 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALLGLCVALLSCSSAAAEFLVGSAPVAPVAALESAAEAGAGTLANPLGTLNPLKLL 60
Db 1 MKLAALLGLCVALLSCSSAAAEFLVGSAPVAPVAALESAAEAGAGTLANPLGTLNPLKLL 60
QY 61 LSSIGIPVNHIIEGSKCVAEGLGPQAVGAVKALKALGALTIVFG 104
Db 61 LSSIGIPVNHIIEGSKCVAEGLGPQAVGAVKALKALGALTIVFG 104
RESULT 15
AEUS9026
ID ABUS9026 standard; protein; 104 AA.
XX
XX AC ABUS9026;
XX
XX DT 16-APR-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein, #163.
XX
XX KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; biosensor; bioreactor; tumour; therapeutic; colon cancer;
KW lung cancer; breast cancer; cancer; gene therapy.
XX
```


Qy 61 LSSIGIPVNHLIEGSKCVAELGPQAVGAVKALKALLGALT VFG 104
 |||||
 Db 61 LSSIGIPVNHLIEGSKCVAELGPQAVGAVKALKALLGALT VFG 104
 |||||

Search completed: June 2, 2004, 20:19:02
Job time : 25.778 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:07:29 ; Search time 67.3906 Seconds

(without alignments)
1966.411 Million cell updates/sec

Title: US-09-700-770-8

Perfect score: 2238

Sequence: 1 MSPPPPLQLLLLLPLLNVE.....ARTRGADLWGGETAQAFPG 420

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_25.*
- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mbc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2238	100.0	420	4 Q8WWD9	Q8WWD9 homo sapien
2	1887	84.3	450	4 Q9UBH3	Q9UBH3 homo sapien
3	1566	70.0	420	11 Q9QX71	Q9QX71 rattus norv
4	1551.5	69.3	419	11 Q9DCS8	Q9DCS8 mus musculu
5	1550.5	69.3	419	11 Q9JW79	Q9JW79 mus musculu
6	1025	45.8	399	13 Q93458	Q93458 podarcis si
7	1018.5	45.5	398	13 Q8JH28	Q8JH28 brachydanio
8	1018.5	45.5	398	13 Q8AWD9	Q8AWD9 brachydanio
9	1014.5	45.3	398	13 P87370	P87370 oncornychu
10	1005.5	44.9	392	5 Q9V313	Q9V313 drosophila
11	1005.5	44.9	399	13 Q9DD89	Q9DD89 brachydanio
12	985.5	44.0	396	13 Q93428	Q93428 chionodraco
13	977	43.7	397	13 Q9W6D4	Q9W6D4 hynobius le
14	974	43.5	395	13 Q8J124	Q8J124 silurus aso
15	966.5	43.2	385	5 Q7Z1E4	Q7Z1E4 bombyx mori
16	949.5	42.4	386	6 Q9BGU5	Q9BGU5 bos taurus

17	324.5	41.3	445	11	Q8C243	Q8C243 mus musculu
18	305.5	40.5	444	5	Q21966	Q21966 caenorhabdi
19	897	40.1	446	5	Q86Q14	Q86Q14 ancylostoma
20	890	39.8	386	5	Q8WR56	Q8WR56 apriona ger
21	887	39.6	446	5	Q9N9H3	Q9N9H3 necator ame
22	374.5	39.1	397	13	Q805F2	Q805F2 xenopus lae
23	871	38.9	409	13	Q804Z9	Q804Z9 xenopus lae
24	865.5	38.7	419	5	Q95VA2	Q95VA2 clonorchis
25	864.5	38.6	397	13	Q805F3	Q805F3 xenopus lae
26	859.5	38.4	495	10	Q9LQZ3	Q9LQZ3 oryza sativ
27	848	37.9	397	13	Q800A0	Q800A0 rana catesb
28	847	37.8	399	13	Q57477	Q57477 sparus aua
29	847	37.8	578	10	Q7XB41	Q7XB41 chlamydomon
30	839	37.5	427	5	P91802	P91802 schistosoma
31	829.5	37.1	429	5	Q26515	Q26515 schistosoma
32	828.5	37.0	514	10	Q8L6A9	Q8L6A9 theobroma c
33	827.5	37.0	452	5	Q8MY58	Q8MY58 brugia mala
34	817	36.5	416	13	Q9DDE2	Q9DDE2 brachydanio
35	804.5	35.9	401	11	Q91X66	Q91X66 mus musculu
36	803.5	35.9	442	5	Q93106	Q93106 ancylostoma
37	803.5	35.9	514	10	Q9FRW9	Q9FRW9 nepenthes a
38	799.5	35.7	404	5	Q8MZF3	Q8MZF3 drosophila
39	797.5	35.6	404	5	Q9V717	Q9V717 drosophila
40	795	35.5	514	10	Q941A2	Q941A2 glycine max
41	792.5	35.4	512	10	Q04593	Q04593 arabidopsis
42	792	35.4	513	10	Q8VYL3	Q8VYL3 arabidopsis
43	785.5	35.1	406	13	P70068	P70068 pagothenia
44	784.5	35.1	504	10	Q93XR0	Q93XR0 ipomoea bat
45	784	35.0	513	10	Q41713	Q41713 vigna ungui

ALIGNMENTS

RESULT 1

Q8WWD9	ID	Q8WWD9	PRELIMINARY;	PRT;	420 AA.
AC	Q8WWD9;				
DT	01-MAR-2002	(Tremblrel. 20, Created)			
DT	01-MAR-2002	(Tremblrel. 20, Last sequence update)			
DT	01-CCT-2003	(Tremblrel. 25, Last annotation update)			
DE	Protapsin A.				
OS	Homo sapiens (Human).				
OC	Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lung;				
RA	Strausberg R.;				
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
CC	- - SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.				
DR	EMBL: BC017842; AAH17842.1; -				
DR	GO: GO:0004194; P:pepsin A activity; IEA.				
DR	GO: GO:0008233; P:peptidase activity; IEA.				
DR	GO: GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro: IPR001461; Peptidase A1.				
DR	InterPro: IPR009007; Pept_A_acid.				
DR	Pfam: PF00026; asp_1.				
DR	PRINTS: PR00792; PEPsin.				
DR	PROSITE: PS00141; ASP_PROTEASE; 2.				
KW	Aspartyl protease; Hydrolase; Protease.				
SQ	SEQUENCE 420 AA; 45374 MW; 05A1B95D68D3F495 CRC64;				

Query Match 100.0%; Score 2238; DB 4; Length 420;

Best Local Similarity 100.0%; Pred. No. 2e-171;

Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPPPPLQLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLRGWREPAELPKLGAPS 60

DB 1 MSPPPPLQLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLRGWREPAELPKLGAPS 60

QY	61	PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWLHH	120
Db	61	PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWLHH	120
QY	121	RFPDKASSSFQANGTKFAIQYGTGRVDGILSSEDKLTIGGKASVIFGEALWEPSSLVFAF	180
Db	121	RFPDKASSSFQANGTKFAIQYGTGRVDGILSSEDKLTIGGKASVIFGEALWEPSSLVFAF	180
QY	181	AHFDGILGLGFPILSVEGVPPMDVLVEQGLLDKPVFSFYLNDRDPPEPDGDELVLGSDP	240
Db	181	AHFDGILGLGFPILSVEGVPPMDVLVEQGLLDKPVFSFYLNDRDPPEPDGDELVLGSDP	240
QY	241	AHYIPPLTFVPTVPAYQWQHMERVKVPGTLTCAKCAAILDTGTSLLTGPTTEERLALH	300
Db	241	AHYIPPLTFVPTVPAYQWQHMERVKVPGTLTCAKCAAILDTGTSLLTGPTTEERLALH	300
QY	301	AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGLGVWFLNTAHDYVVIQTTRNGVRLCLSGFQA	360
Db	301	AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGLGVWFLNTAHDYVVIQTTRNGVRLCLSGFQA	360
QY	361	LDVPPAGPFWILGDVFLGTGYVAVFDRGDMKSSARVGLARTRGADLGHGETAQAPFG	420
Db	361	LDVPPAGPFWILGDVFLGTGYVAVFDRGDMKSSARVGLARTRGADLGHGETAQAPFG	420
RESULT 2			
QY	Q9UHB3	PRELIMINARY; PRT; 450 AA.	
AC	Q9UHB3		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Aspartyl protease 3 (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20057170; PubMed=10591213;		
RA	Yan R., Bienkowski M.J., Shuck M.B., Miao H., Tory M.C., Pauley A.M.,		
RA	Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,		
RA	Tomaselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.B.;		
RT	"Membrane-anchored aspartyl protease with Alzheimer's disease beta-		
RT	secretase activity.;"		
RL	Nature 402:533-537(1999).		
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.		
DR	EMBL; AF200344; AAF17080.1; -.		
DR	HSSP; P00794; 4CMS.		
DR	MEROPS; A01.972; -.		
DR	GO; GO:0016020; C:membrane; TAS.		
DR	GO; GO:0004194; F:pepsin A activity; NAS.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; TAS.		
DR	InterPro; IPR001969; Aspartase AS.		
DR	InterPro; IPR001461; Peptidase A1.		
DR	InterPro; IPR009007; Pept_A_acid.		
DR	Pfam; PF00026; asp; 1.		
DR	PRINTS; PR00792; PEPIN.		
DR	PROSITE; PS00141; ASP PROTEASE; 2.		
KW	Aspartyl protease; Hydrolase; Protease.		
FT	NON TER 450		
SQ	SEQUENCE 450 AA; 48576 MW; B7731C85E106C0DD CRC64;		
Query Match			
Best Local Similarity 84.3%; Score 1887; DB 4; Length 450;			
Matches 360; Conservative 16; Mismatches 44; Indels 0; Gaps 0;			
QY	1	MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQPGRTINLIRGWRPAELPKLGAPS	60
Db	1	MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQPGRTINLIRGWRPAELPKLGAPS	60
QY	61	PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWLHH	120

Db	61	PGDKPASVLSKFLDAQYFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWFHH	120
QY	121	RDPKASSSFQANGTKFAIQYGTGRVDGILSSEDKLTIGGKASVIFGEALWEPSSLVFAF	180
Db	121	RNPKNASSFKPSGCTKFAIQYGTGRVDGILSSEDKLTIGGKASVIFGEALWESSLVFTV	180
QY	181	AHFDGILGLGFPILSVEGVPPMDVLVEQGLLDKPVFSFYLNDRDPPEPDGDELVLGSDP	240
Db	181	SRPDGILGLGFPILSVEGVPPMDVLVEQGLLDKPVFSFYFNDRDPPEVADGDELVLGSDP	240
QY	241	AHYIPPLTFVPTVPAYQWQHMERVKVPGTLTCAKCAAILDTGTSLLTGPTTEERLALH	300
Db	241	AHYIPPLTFVPTVPAYQWQHMERVKVSGRLTLCAGCAAILDTGTPVIVGPTTEERLALH	300
QY	301	AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGLGVWFLNTAHDYVVIQTTRNGVRLCLSGFQA	360
Db	301	AAIGGIPLLAGEYIIRCSIEPKLPVAVSLLIGGVWFLNTAQDYVVIQFAGDVRCLSGFRA	360
QY	361	LDVPPAGPFWILGDVFLGTGYVAVFDRGDMKSSARVGLARTRGADLGHGETAQAPFG	420
Db	361	LDIASPPVPWILGDVFLGTGYVAVFDRGDMKSGARVGLARPRGADLGRRETAQAQYRG	420
RESULT 3			
QY	Q9QX71	PRELIMINARY; PRT; 420 AA.	
AC	Q9QX71		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Napsin.		
GN	NAP.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20461778; PubMed=10858550;		
RA	Schauer-Vukasinovic V., Wright M.B., Breu V., Giller T.;		
RT	"Cloning, expression and functional characterization of rat napsin.;"		
RL	Biochim. Biophys. Acta 1492:207-210(2000).		
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.		
DR	EMBL; AJ251299; CAB65392.1; -.		
DR	HSSP; P00797; 2REN.		
DR	MEROPS; A01.049; -.		
DR	GO; GO:0004194; F:pepsin A activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001969; Aspartase AS.		
DR	InterPro; IPR001461; Peptidase A1.		
DR	InterPro; IPR009007; Pept_A_acid.		
DR	Pfam; PF00026; asp; 1.		
DR	PRINTS; PR00792; PEPIN.		
DR	PROSITE; PS00141; ASP PROTEASE; 2.		
KW	Aspartyl protease; Hydrolase; Protease.		
SQ	SEQUENCE 420 AA; 45629 MW; A6851C6A2F7DED7C CRC64;		
Query Watch			
Best Local Similarity 70.4%; Score 1566; DB 11; Length 420;			
Matches 299; Conservative 39; Mismatches 77; Indels 10; Gaps 5;			
QY	1	MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQPGRTINLIRGWRPAELPKLGAP	59
Db	1	MLPPELL--LLLCVLGNLEPA-ATLIRVPLRIRHPGHRIFSPLYGWEQRAELSR--TP	55
QY	60	SPGDPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAEDTGSNNLWVPBRRCHFFSVPCWLH	119
Db	56	TSGGKTAFAVPLSKFNTQYFGDIGLTPQNFTVVDGSSNLWVPSTRCHFFSLACWFH	115
QY	120	HRFPDKASSSFQANGTKFAIQYGTGRVDGILSSEDKLTIGGKASVIFGEALWEPSSLVFA	179
Db	116	HRFNPKASSFRPNGTKFAIQYGTGRVLSRDNLTIIGGIHNSVTGFEALWEPSSLVFA	175


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QY 180 FAHFDGILGFPILSVGVRPMDVLVQGLLDKPVFSFYLNDRDPEPDGGLVLGSSD 239
Db 176 LARFDGILGFPILSVGVRPMDVLVQGLLDKPVFSFYLNDRDPEPDGGLVLGSSD 235
QY 240 PAHYIPLTFVPTVTPAYVQIHMERYKVGFGTLCAKCAAILDTGSLTGTETIRAL 299
Db 236 PDHYVPLTFVPTVTPAYVQIHMERYKVGFGTLCAKCAAILDTGSLTGTETIRAL 295
QY 300 HAAIGIPILAGHYIILCSBIPKLPVAVSFLGGVWNLTAHDYVQIOTTRNGVPLCLSGFQ 359
Db 296 NKAAGVGFLLTGQYLICQCKIPBLPTVSFSLGGVWNLTAHDYVQIOTTRNGVPLCLSGFQ 355
QY 360 ALDVPVPPAGFWILGDFVLTGYVAVFDRGDMKSSARVGLARATRGADLWGSETAQAF 418
Db 356 ALDIPKPEGLWILGDFVLTGYVAVFDRGDMKSSARVGLARATRGADLWGSETAQAF 415
QY 419 ---PG 420
Db 416 RRRFG 420

RESULT 4
Q9DCS8 PRELIMINARY; PRT; 419 AA.
AC Q9DCS8;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Kidney-derived aspartic protease-like protein.
GN KDAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schram L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaehizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AK002520; BAB2158.1; -.
DR HSP; P00797; 2REN.
DR MGD; MGI:109365; Kdap.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; Approtease AS.
DR InterPro; IPR001461; Peptidase A1.
DR InterPro; IPR009007; Pept_A acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP PROTEASE; 2.
KW Aspartyl protease; Hydrolase; Protease.

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SQ SEQUENCE 419 AA; 45504 MW; 715EC5472280003B CRC64;
Query Match 69.3%; Score 1551.5; DB 11; Length 419;
Best Local Similarity 70.1%; Pred. No. 2.7e-116;
Matches 295; Conservative 37; Mismatches 80; Indels 9; Gaps 3;

QY 7 LQPLALLLPL---NVEPSGATLIRPLHRVQPGRTTLMNLGRWEPAPLKLGAAPSGD 63
Db 1 MSPPLALLLCLLGNLEPEAKLIRVPLQRIHLGRIILNPLNGWEQLAELSR--TSTSG 58
QY 64 KFIPLSYNRDVQVFGELIGTTPONFTVADTSSNLWVSRRCFFSVPCWLHHRD 123
Db 59 NPSFVPLSKFMNTQVFTGLTTPQNTFTVFDTGSSNLWVSTRCHFFSLACWFHREN 118
QY 124 PRASSFOANGTKFAIOYGTGRVDGLISBDKLTIGGKASVIFGREALWEPISLFAFAHF 183
Db 119 PRASSFRNGTKFAIOYGTGRISGLSDNLTIGGIHDAFTVFGREALWEPISLFAFAHF 178
QY 184 DGIILGFPILSVGVRPMDVLVQGLLDKPVFSFYLNDRDPEPDGGLVLGSSDPAHY 243
Db 179 DGIILGFPFLAVGGVQPPDLAMVEQGLLEKPVFSFYLNDRDSESGDGLVLGSSDPAHY 238
QY 244 IPLLTFVPTVTPAYVQIHMERYKVGFGTLCAKCAAILDTGSLTGTETIRALHAI 303
Db 239 VPPLTFVPTVTPAYVQIHMERYKVGFGTLCAKCAAILDTGSLTGTETIRALHAI 298
QY 304 GGIPLLAGFVILCSBIPKLPVAVSFLGGVWNLTAHDYVQIOTTRNGVPLCLSGFOALDV 363
Db 299 GGYPLNGQVFFQCKTPTLPVSVFHLGGVWNLTAHDYVQIOTTRNGVPLCLSGFOALDI 358
QY 364 PPPAGFPWILGDFVLTGYVAVFDRGDMKSSARVGLARATRGADLWGSETAQAF----P 419
Db 359 PNAAGPLWILGDFVLTGYVAVFDRGDMKSSARVGLARATRGADLWGSETAQAFKRRP 418
QY 420 G 420
Db 419 G 419

RESULT 5
Q9JMW9 PRELIMINARY; PRT; 419 AA.
AC Q9JMW9;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Aspartic proteinase family member similar to renin.
GN KDAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Takenaka M., Imai E.;
RA Hori M., Kawamoto S., Okubo K.;
RT "Isolation of genes identified in mouse renal proximal tubule by comparing different gene expression profiles.";
RL Kidney Int. 53:562-572(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AB038144; BAA90785.1; -.
DR HSP; P00797; 2REN.
DR MGD; MGI:109365; Kdap.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

```


Db	359	MDIPPSG-LWTLGDVFIGYTYTFDR-----ENDRVGLAKAK	395
RESULT 14			
Q8J124			
ID	Q8J124	PRELIMINARY;	PRT; 395 AA.
AC	Q8J124;		
DT	01-CCT-2002 (T-EMBLrel. 22, Created)		
DT	01-CCT-2002 (T-EMBLrel. 22, Last sequence update)		
DT	01-CCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Cathepsin D preproprotein.		
OS	Silurus asotus (Namazu) (Amur catfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;		
OC	Siluridae; Silurus.		
OX	NCBI_TaxID=30991;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21863985; PubMed=11821259;		
RA	Cho J.H., Park I.Y., Kim H.S., Lee W.T., Kim M.S., Kim S.C.;		
RT	"Cathepsin D produces antimicrobial peptide parasin I from histone H2A in the skin mucosa of fish.";		
RL	FASEB J. 16:429-431(2002);		
DR	EMBL; AF396662; AAM62283.1; -.		
DR	GO; GO:0004194; F:pepsin A activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001969; Asparticase AS.		
DR	InterPro; IPR001461; Peptidase A1.		
DR	InterPro; IPR009007; Pept_A_acid.		
DR	Pfam; PF00026; asp; 1.		
DR	PRINTS; PR00792; PEPSIN.		
DR	PROSITE; PS00141; ASP_PROTEASE; 2.		
SQ	SEQUENCE 395 AA; 43030 MW; A731DBDE43664573 CRC64;		
Query Match	43.5%;	Score 974;	DB 13; Length 395;
Best Local Similarity	48.3%;	Pred. No. 6.1e-70;	
Matches 195;	Conservative	66;	Mismatches 119; Indels 24; Gaps 6;
QY	10	LLLLLLPLNVPESGATLIRPLHRVQGRRTIN-----LLRGWRPAPLPLKLG-----	57
Db	3	LACLLLVFIATADALVRIFLKKFRSIRRTMSDGRAVESRGNQTKY- NLGVTKNF	61
QY	58	APSGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFTVADTGSNNLWVPSRCHFSVPCW	117
Db	62	GTP-----ETLKNYLDAYYGEIGLGTPTVQTTVFDTSNNLWVPSVHCSTDIACL	115
QY	118	LHHRDPKASSSQANGKFAIQYGRVDGILSGDKLTIGIKGASVIFGEALWEPGLV	177
Db	116	LHHKNGAKSSTYVKNGTAFALQYSGSLGSLGSDVCSIGDIAVEKQIFGEAIKPGVA	175
QY	178	FAFAHFDGILGILGFPILSVGVPRPMDVLVQGLDQKPVFSFYLNRPDEPDGGLVLGG	237
Db	176	FLAAKFDGLGMAYPRIADVGV-PVFDMMQKKFKNVFSFYLNRPDTPQGGELLGG	234
QY	238	SDPAHYIPLTFVPTVYQWQHMERVKVPGTLCAKGAAILDTGTLTSLTGTEIR	297
Db	235	TDPEYTGDFHYVNTTQAYQWQHMDGMSIGSGLSCNGGCEAVDTGTLTSLTGPAEVK	294
QY	298	ALHAAGGIPILAGVYIILCSIEPKLPVAVSFLGGVWFNLTAHDYVIOITTRNGVRLCLSG	357
Db	295	ALQKAIKAIPLIQGEWYDCKVPSLPTISFNLGGQTYTLTGEQYILKESQAGREICLSG	354
QY	358	FOALDVPVPPAGFWTLGDVFLGTGYVAVFDRGDMKSSARVGLARA	401
Db	355	FWALDIPPPAGFLWLGDFVIGQYTFDR-----ENNQVGFAPA	394
RESULT 15			
Q721E4			
ID	Q721E4	PRELIMINARY;	PRT; 385 AA.
AC	Q721E4;		
DT	01-OCT-2003 (T-EMBLrel. 25, Created)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last sequence update)		

Db	292	VEVALQKALGAPFLIOGEYMWNCDTVPSLVSFTVGGQVYTLTGEOYILKVTQAGKTM	351
QY	354	CLSGFQALDVPVPPAGFWTLGDVFLGTGYVAVFDRGDMKSSARVGLAPAR	402
Db	352	CLSGFMGLDIPAPAGPLWILGDVFMQYTYTFDR-----DANRVGFAKAK	396
RESULT 13			
Q9W6D4			
ID	Q9W6D4	PRELIMINARY;	PRT; 397 AA.
AC	Q9W6D4;		
DT	01-NOV-1999 (T-EMBLrel. 12, Created)		
DT	01-NOV-1999 (T-EMBLrel. 12, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Cathepsin D (EC 3.4.23.5).		
OS	Hynobius leechii (Korean salamander).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Caudata; Cryptobranchoidea; Hynobiidae; Hynobius.		
OX	NCBI_TaxID=113391;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20358712; PubMed=10902906;		
RA	Ju B.G., Kim W.S.;		
RT	"Cloning of a cDNA encoding cathepsin D from salamander, Hynobius leechii, and its expression in the limb regenerates.";		
RL	DNA Seq. 11:21-28(2000).		
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.		
DR	EMBL; AF115925; AAD33219.1; -.		
DR	HSSP; P07339; 1LYB.		
DR	MEROPS; A01.009; -.		
DR	GO; GO:0004192; F:cathepsin D activity; IEA.		
DR	GO; GO:0004194; F:pepsin A activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001969; Asparticase AS.		
DR	InterPro; IPR001461; Peptidase A1.		
DR	InterPro; IPR009007; Pept_A_acid.		
DR	Pfam; PF00026; asp; 1.		
DR	PRINTS; PR00792; PEPSIN.		
DR	PROSITE; PS00141; ASP_PROTEASE; 2.		
KW	Aspartyl protease; Hydrolase; Protease.		
SQ	SEQUENCE 397 AA; 42855 MW; 75CB1EA482D3DFE9 CRC64;		
Query Match	43.7%;	Score 977;	DB 13; Length 397;
Best Local Similarity	48.3%;	Pred. No. 3.5e-70;	
Matches 194;	Conservative	70;	Mismatches 116; Indels 22; Gaps 5;
QY	10	LLLLLLPLNVPESGATLIRPLHRVQGRRTINLLRGWRPAPLPLKLGAPSPGDKPIFVP	69
Db	7	LLLLAPLLALHA--MVRPLTKFRSIRHTLTEAGG-----DIXNLVATSDQVKNCP	58
QY	70	-----LSNYRDVQYGEIGLGTTPQNTFTVADTGSNNLWVPSRCHFSVPCWLH	120
Db	59	KTQQTPELKNYLDAYYGEICIGTPPQCTVFDTSNNLWVPSVHCSTDIACLVRP	118
QY	121	RDPKASSSQANGKFAIQYGRVDGILSGDKLTIGIKGASVIFGEALWEPGLV	180
Db	119	KYDSSSSSTYVKNGTAFALQYSGSLGSLGSDVCSIGDIAVEKQIFGEAIKPGVAFTA	178
QY	181	AHFDGILGILGFPILSVGVPRPMDVLVQGLDQKPVFSFYLNRPDEPDGGLVLGGSDP	240
Db	179	AKFDGILGMAYPRIADVGVTKLVEKNVFSFYLNRPDTPRPGELLGGTDP	238
QY	241	AHYIPLTFVPTVYQWQHMERVKVPGTLCAKGAAILDTGTLTSLTGTEIRALH	300
Db	239	NYTGTFTYLNTPKAYQWQHMDQGLTGKGCCEAIVDTGTLTSLTGSAEVTALQ	298
QY	301	AAIGGIPILAGVYIILCSIEPKLPVAVSFLGGVWFNLTAHDYVIOITTRNGVRLCLSGFOA	360
Db	299	KALGAIPLIOGEYMWPCDKVPSLPTISFNLGGQTYTLTGEQYILKESQAGHTICLSGFMG	358
QY	361	LDVPPVPPAGFWTLGDVFLGTGYVAVFDRGDMKSSARVGLAPAR	402

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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:05:19 ; Search time 16.3371 seconds
(without alignments)
1338.637 Million cell updates/sec

Title: US-09-700-770-8
Perfect score: 2238
Sequence: 1 MSPPPPLQLPLLLLLLPLLNVE.....ARTRGADLGMGTAAQPPG 420

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	2232	99.7	1 NAPI_HUMAN	O96009 homo sapien
2	1560.5	69.7	1 KRAP_MOUSE	O09043 mus musculus
3	1030	46.0	1 CATD_CHICK	Q05744 gallus gall
4	1019.5	45.6	1 CATD_CLUHA	Q9dex3 cluhea hare
5	1015	45.4	1 CATD_HUMAN	P07339 homo sapien
6	1005	44.9	1 CATD_RAT	P24268 rattus norv
7	992.5	44.3	1 CATD_MOUSE	P18242 mus musculus
8	967.5	43.2	1 CATD_BOVIN	P80209 bos taurus
9	964.5	43.1	1 ASPP_AEDAE	Q03168 aedes aegypt
10	944	42.2	1 CATD_PIG	P00795 sus scrofa
11	922.5	41.2	1 CATD_SHEEP	Q9mz88 ovis aries
12	878	39.2	1 CATE_MOUSE	P70269 mus musculus
13	869	38.8	1 CATE_HUMAN	P14091 homo sapien
14	867	38.7	1 CATE_RAT	P18228 rattus norv
15	848.5	37.9	1 CATE_RABIT	P43159 oryctolagus
16	830	37.1	1 ASPR_HORVU	P42210 hordeum vul
17	808.5	36.1	1 RENS_MOUSE	P00796 mus musculus
18	806.5	36.0	1 CATE_CAVPO	P25796 cavia porce
19	804	35.9	1 APR1_ORYSA	Q42456 oryza sativ
20	797	35.6	1 REN1_MOUSE	P06281 mus musculus
21	783	35.0	1 REN1_SHEEP	P52115 ovis aries
22	781	34.9	1 CYP1_CYNCA	P08424 cynara card
23	779	34.8	1 REN1_RAT	P08424 rattus norv
24	779	34.8	1 REN1_HUMAN	P00797 homo sapien
25	779	34.8	1 REN1_PANTR	P60016 pan troglod
26	773.5	34.6	1 ASPR_ORYSA	P42211 oryza sativ
27	769.5	34.4	1 ASPR_CUCPE	O04057 cucurbita p
28	767.5	34.3	1 ASPR_MACFU	P27678 macaca fusc
29	765.5	34.2	1 PEP4_MACMU	P11489 macaca mula
30	759.5	33.9	1 PEP4_HUMAN	P00790 macaca mla
31	757.5	33.8	1 PEP2_MACFU	P27677 macaca fusc
32	756	33.8	1 ASF3_CAEBL	P55956 caenorhabdi
33	755.5	33.8	1 PEP1_MACFU	P03954 macaca fusc

34	735.5	32.9	386	1	PEPA_PIG	P00791 sus scrofa
35	735	32.8	387	1	PEP2_RABIT	P27821 oryctolagus
36	733	32.8	387	1	PEP4_RABIT	P28713 oryctolagus
37	717	32.0	387	1	PEP1_RABIT	P28712 oryctolagus
38	707.5	31.6	383	1	PEPE_CHICK	P16476 gallus gall
39	702	31.4	387	1	PEPA_CALJA	Q9n2d4 callithrix
40	700	31.3	396	1	CARP_NEUCR	Q01294 neurospora
41	687.5	30.7	394	1	PEPC_CAVPO	Q64411 cavia porce
42	685	30.6	387	1	PEP3_RABIT	P27822 oryctolagus
43	685	30.6	405	1	CARP_YEAST	P07267 saccharomyc
44	680.5	30.4	392	1	PEPC_RAT	P04073 rattus norv
45	679.5	30.4	381	1	CHYM_SHEEP	P18276 ovis aries

ALIGNMENTS

RESULT 1
NAPI_HUMAN
ID NAPI_HUMAN STANDARD; PRT; 420 AA.
AC O96009;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Napsin 1 precursor (EC 3.4.23.-) (Napsin A) (NAPA) (TA01/TA02)
DE (Aspartyl protease 4) (Asp 4) (ASP4).
GN NAPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Lung;
RX MEDLINE=95092989; PubMed=9877162;
RA Tatnell P.J., Powell D.J., Hill J., Smith T.S., Tew D.G., Kay J.;
RT "Napsins: new human aspartic proteinases. Distinction between two
RT closely related genes.";
RL FEBS Lett. 441:43-48(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Koelsch G., Wu S., Henthorn J., Tang J., Lin X.;
RT "New human aspartic proteases napsin 1 and napsin 2: molecular
RT cloning and intracellular localization of napsin 1.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Fetal lung;
RX MEDLINE=20047840; PubMed=10580105;
RA Chuman Y., Bergman A.-C., Ueno T., Saito S., Sakaguchi K.,
RA Alaya A.A., Franzen B., Bergman T., Arnott D., Auer G., Appella E.,
RA Joernvall H., Linder S.;
RT "Napsin A, a member of the aspartic protease family, is abundantly
RT expressed in normal lung and kidney tissue and is expressed in lung
RT adenocarcinomas.";
RL FEBS Lett. 462:129-134(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Bienkowski M.J., Shuck M.E., Slightom J.L., Drong R.F.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in processing of pneumocyte surfactant
CC precursors.
CC -!- TISSUE SPECIFICITY: Expressed predominantly in adult lung (type II
CC pneumocytes) and kidney and in fetal lung. Low levels in adult
CC spleen and very low levels in peripheral blood leukocytes.
CC -!- SIMILARITY: Belongs to peptidase family A1.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 16
FT PROPEP 17 ?
FT CHAIN ? 419
FT ACT SITE 91
FT BY SIMILARITY.
FT ACT SITE 278
FT BY SIMILARITY.
FT DISULFID 104
FT BY SIMILARITY.
FT DISULFID 269
FT BY SIMILARITY.
FT DISULFID 312
FT BY SIMILARITY.
FT CARBOHYD 85
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 419 AA; 45544 MW; 715ED4532791143E CRC64;

Query Match 69.7%; Score 1560.5; DB 1; Length 419;
Best Local Similarity 70.3%; Pred. No. 3.1e-118;
Matches 296; Conservative 37; Mismatches 79; Indels 9; Gaps 3;

QY 7 LQPLLLLLP---NVEPSGATLIRPLHRVQGRRTLLRGRBPAELPKLGAPSGD 63
DB 1 MSPLLLALLCLLGNLEPEPAKLIRVPLQRIHLGHRILNPLNGWEQLAELSR--TSTGG 58
QY 64 KPIFVPLSNRYDQYFGEIGLGTTPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123
DB 59 NPSFVPLSKPMNTQYFGTIGLGTTPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 118
QY 124 PKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWPSLVFAPAHF 183
DB 119 PKASSFRPNGTFAIQYGTGRVLSQNLGILGTHDAFVTFGEALWPSLVFAPAHF 178
QY 184 DGILGLFPILSEGVPPMDVLEQGLDKPVSFVYLNDRDPEPDGELVLGSSDPAHY 243
DB 179 DGILGLFPILSEGVPPMDVLEQGLDKPVSFVYLNDRDPEPDGELVLGSSDPAHY 238
QY 244 IPPLTFVPTVPAYWQIHMVSKVPGTLTCAKCAAILDTGTLTGPEEIRALHAAI 303
DB 239 VPPLTFVPTVPAYWQIHMVSKVPGTLTCAKCAAILDTGTLTGPEEIRALHAAI 298
QY 304 GGIPLLAGIYILCEIPKPAVSLFGLGVWVFNLTADHYVIQTRNGVRLCLSGFQALDV 363
DB 299 GGYPLFNGQYFIQCKTPTLPVPSFHLGVWVFNLTADHYVIQTRNGVRLCLSGFQALDI 358
QY 364 PPAPGPKWILGDVFLGTVAVFDRGDMKSSARVGLARFAGDLGWGTAQAF---P 419
DB 359 PKPAGPLWILGDVFLGTVAVFDRGDMKSSARVGLARFAGDLGWGTAQAF---P 418
QY 420 G 420
DB 419 G 419

RESULT 3
CATD CHICK
ID CATD CHICK STANDARD; PRT; 398 AA.
AC Q05744;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DB Cathepsin D precursor (EC 3.4.23.5).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 64-97.
RC TISSUE=Pollicle;
RX MEDLINE=93039672; PubMed=1418623;
RA Retek H., Steyer E., Sanders E.J., Nimpf J., Schneider W.J.;
RT "Molecular cloning and functional characterization of chicken
cathepsin D, a key enzyme for yolk formation."

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RL DNA Cell Biol. 11:661-672(1992).
CC !- FUNCTION: Cathepsin D is an acid protease active in intracellular
CC protein breakdown. In chicken it is a key enzyme for yolk
CC formation as it is capable of catalyzing intra oocytic break down
CC of protein components of both vitellogenin and VLDL.
CC !- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
CC chain of insulin.
CC !- SUBUNIT: Consists of a light chain and a heavy chain.
CC !- SUBCELLULAR LOCATION: Lysosomal.
CC !- TISSUE SPECIFICITY: Oocytic yolk, preovulatory follicles, liver.
CC !- SIMILARITY: Belongs to peptidase family A1.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; S49650; AAB24157.1; -
CC PIR; I51185; I51185.
CC HSP; P07339; ILYB.
CC MEROPS; A01.009; -.
CC InterPro; IPR001969; Aspprotease_AS.
CC InterPro; IPR009007; Pept_A_acid.
CC InterPro; IPR001461; Peptidase_A1.
CC Pfam; PF00026; asp; 1
CC PRINTS; PRO0792; PEPsin.
CC PROSITE; PS00141; ASP_PROTEASE; 2.
CC Hydrolase; Aspartyl 20
CC SIGNAL 21 63
CC PROPEP 21 63
CC CHAIN 64 398
CC CHAIN 64 157
CC CHAIN 158 398
CC ACT SITE 96 96
CC ACT SITE 283 283
CC DISULFID 109 116
CC DISULFID 274 278
CC DISULFID 317 354
CC CAREOHYD 133 133
CC CAREOHYD 251 251
CC SEQUENCE 398 AA; 43298 MW; 584C99E2755AA2B1 CRC64;

Query Match 46.0%; Score 1030; DB 1; Length 398;
Best Local Similarity 50.0%; Pred. No. 1.5e-75;
Matches 208; Conservative 57; Mismatches 115; Indels 36; Gaps 7;

QY 1 MSPPLQLPQLLLPLLNVPSPGATLIRPLHRVQGRRTLLRGRBPAELPKLGA-- 58
DB 1 MAPRGLL--VLLLLAL--VGPC-AALIRIPLTKFTSTRMLT-----EVGSEIPDMNAIT 50
QY 59 -----PSPGDKPIFVPLSNRYDQYFGEIGLGTTPQNFTVAFDTGSSNLWV 104
DB 51 QFLKFLGFADLABPTP-----EILKNYMDAQYGEIGLGTTPQNFTVAFDTGSSNLWV 104
QY 105 PSRECHFFSVPCWLHHRFDPKASSSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKIGAS 164
DB 105 PSVCHLLDACLHLHKYDASKSTYYVENGTEFAIHVGTGSLSGFLSQDVTYVTLGNLKN 164
QY 165 VIFGEALWERSLVFAFAHFDGILGFPILSVGEVGRPPMDVLEQGLDKPVSFVYLNDRD 224
DB 165 QIFGEAVKQPGITFAIAKFDGILGMAFPRISSVDKVTFFFDNMVQKLIKIEKIFSYLNDRD 224
QY 225 PEPDGGELVLGSSDPAHYIPPLTFVPTVPAYWQIHMVSKVPGTLTCAKCAAILDT 284
DB 225 PTAQPGGELLGGTDPKYSGDFSWVNVTRKAYQVHMDSVDVANGTLTCKGCGEALVDT 284
QY 285 GTSILITGTEETIRALHAAGIGIPILAGYIILCEIPKPAVSLFGLGVWVFNLTADHYVI 344
DB 285 GTSILITGTEETIRALHAAGIGIPILAGYIILCEIPKPAVSLFGLGVWVFNLTADHYVI 344

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [5]
RN SEQUENCE OF 1-22 FROM N.A.
RP MEDLINE=94085791; PubMed=8262386;
RX May F.E., Smith D.J., Westley B.R.;
RA "The human cathepsin D-encoding gene is transcribed from an estrogen-
RT regulated and a constitutive start point.";
RL Gene 134:277-282(1993).
RN [6]
RN SEQUENCE OF 1-22 FROM N.A.
RX MEDLINE=95021301; PubMed=7935485;
RA Augereau P., Miralles F., Cavailles V., Gaudelet C., Parker M.,
RA Rochefort H.;
RA "Characterization of the proximal estrogen-responsive element of
RT human cathepsin D gene.";
RL Mol. Endocrinol. 8:693-703(1994).
RN [7]
RN SEQUENCE OF 170-180.
RP TISSUE=Liver;
RX Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RL Submitted (JUN-1992) to Swiss-Prot.
RN [8]
RN CARBOHYDRATE-LINKAGE SITE ASN-263.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
RN [9]
RN VARIANT VAL-58.
RX MEDLINE=20179010; PubMed=10716266;
RA Papassotiropoulos A., Bagli M., Kurz A., Kornhuber J., Forstl H.,
RA Maier W., Pauls J., Lautenschlager N., Heun R.;
RT "A genetic variation of cathepsin D is a major risk factor for
RT Alzheimer's disease.";
RL Ann. Neurol. 47:399-403(2000).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RP TISSUE=Spleen;
RX MEDLINE=93223670; PubMed=8467789;
RA Metcalf P., Fusek M.;
RT "Two crystal structures for cathepsin D: the lysosomal targeting
RT signal and active site.";
RL EMBO J. 12:1293-1302(1993).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP TISSUE=Liver;
RX MEDLINE=93342076; PubMed=8393577;
RA Baldwin E.T., Bhat T.N., Gulnik S., Hosur M.V., Sowder R.C. II,
RA Cachau R.E., Collins J., Silva A.M., Erickson J.W.;
RT "Crystal structures of native and inhibited forms of human cathepsin
RT D: implications for lysosomal targeting and drug design.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6796-6800(1993).
CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
CC Involved in the pathogenesis of several diseases such as breast

CC cancer and possibly Alzheimer's disease.
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
CC chain of insulin.
CC -!- SUBUNIT: Consists of a light chain and a heavy chain.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- POLYMORPHISM: The Val-58 allele is significantly overrepresented
CC in demented patients (11.8%) compared with nondemented controls
CC (4.9%). Carriers of the Val-58 allele have a 3.1-fold increased
CC risk for developing AD than noncarriers.
CC -!- SIMILARITY: Belongs to peptidase family A1.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M11233; AAB59529.1; -;
CC EMBL; X05344; CRA28955.1; -;
CC EMBL; M63138; AAS1922.1; -;
CC EMBL; M63134; AAS1922.1; JOINED.
CC EMBL; M63135; AAS1922.1; JOINED.
CC EMBL; M63136; AAS1922.1; JOINED.
CC EMBL; M63137; AAS1922.1; JOINED.
CC EMBL; BC016320; AAH16320.1; -;
CC EMBL; L12980; AAL16314.1; -;
CC EMBL; S74689; AAD14156.1; -;
CC EMBL; S52557; AAD13868.1; -;
CC PIR; A25771; KKHUO.
CC PDB; 1LYA; 31-JAN-94.
CC PDB; 1LYB; 31-JAN-94.
CC PDB; 1LYW; 22-JUL-99.
CC MEROPS; A01.009; -;
CC SWISS-2DPAGE; P07339; HUMAN.
CC Siera-2DPAGE; P07339; -;
CC Genew; HGNC:2529; CTSD.
CC MIM; 116840; -;
CC GO; GO:0004192; F:cathepsin D activity; TAS.
CC InterPro; IPR001969; Aspartate AS.
CC InterPro; IPR009007; Pept A acid.
CC InterPro; IPR001461; Peptidase_A1.
CC Pfam; PF00026; asp; 1.
CC PRINTS; PR00792; PEPsin.
CC PROSITE; PS00141; ASP_PROTEASE; 2.
CC Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Signal; Zymogen;
CC Polymorphism; Alzheimer's disease; 3D-structure.
CC SIGNAL 1 18
CC PROPEP 19 64
CC CHAIN 65 412
CC CHAIN 65 412
CC CHAIN 169 412
CC ACT SITE 97 97
CC ACT SITE 295 295
CC DISULFID 91 160
CC DISULFID 110 117
CC DISULFID 286 290
CC DISULFID 329 366
CC CARBOHYD 134 134
CC CARBOHYD 263 263
CC VAR-ANT 58 58
CC
CC STRAND 67 74
CC TURN 75 77
CC STRAND 78 85
CC TURN 86 89
CC STRAND 90 97
CC TURN 98 99
CC STRAND 103 107

N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
A -> V (ASSOCIATED WITH INCREASED RISK IN
AD; POSSIBLY INFLUENCES SECRETION AND
INTRACELLULAR MATURATION; dbSNP:17571).
/FTid=VAR_011621.

```

FT TURN 108 109
FT TURN 112 113
FT HELIX 115 118
FT TURN 119 119
FT STRAND 123 123
FT HELIX 125 127
FT TURN 129 130
FT STRAND 132 141
FT STRAND 146 158
FT STRAND 172 184
FT HELIX 188 192
FT STRAND 197 200
FT HELIX 204 206
FT HELIX 208 210
FT HELIX 214 220
FT TURN 221 222
FT STRAND 228 233

Query Match 45.4%; Score 1015; DB 1; Length 412;
Best Local Similarity 46.9%; Pred. No. 2.6e-74;
Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

QY 1 MSPPPQLPQLLLPLLVNVEGSGATLIRIPHRVQPGRTNLLRGWRE-----PAELP 54
DB 1 MQPSSLPLALCLL-----AAPASA-LVRIPLHKFTSIRRTMSEVGGSVEDLIAGKPVSKY 55

55 KLGAPSPGDKPIFVPLSNRYDVQVFGELGTGTPQNETVAFDTGSSNLWVPSRRCHFFSV 114
DB 56 SQAVPAVTEGPIDVPLKYNDAQYGEIGTGPPOCFVTFVDTGSSNLWVPSIRHCKLDDI 115

115 PCWLHHRDPPKASSSFQANGKFAIQYGTGRVDGILSEDKLTI-----GGIKGA 163
DB 116 ACWIHKYNSDKSSYVKNKGSFSDIHYGSGLSGLYSDTVSVPCQSASSASALGGVKVE 175

164 SVIFGEALWERSLVPAFAHFDGILGPPILSVVEGVRPMDVLVEQGLDKPVSFYLR 223
DB 176 RQVGEATKQEGITFAAKFDGILGMAYPRISVNNVLFVFDNMQQLVDQNIFFSYLSR 235

224 DPEPDGELVGGSDPAHYTPPLTFVPTVPAYQIHWKVKVGFGLTCAKGCACALID 283
DB 236 DPDAQGGELMGGDSKYKYSGLSYLVNTRKAYQVHLDQVEVASGTLCKEGCEAIVD 295

284 TGTSLITPTERIRALHAAGIGPIPLAGEYIILCSIEIPKLPVAVSFLGGMWFLNFAHDYV 343
DB 296 TGTSLWVGVDVRELOKAGAVPLIQGEYMPICEKVSFTLPAITLKGKGKVLSPEDYT 355

344 IOTTNGVRLCLSGQALDVPVPPAGPFWLGVFTGYVAVEDRGMKSSARVGLARA 401
DB 356 LKVSQAGKTLCLSGPMGMDIPPPSGELWILGDFVFGYTYTFDR-----DNNRVGFAEA 409

RESULT 6
CATD RAT
ID CATD RAT STANDARD; PRT; 407 AA.
AC P24268;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN CTSD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=pituitary;
RX MEDLINE=91057150; PubMed=2243802;
RT Birch N.P., Loh Y.P.;
RT "Cloning, sequence and expression of rat cathepsin D.";
RL Nucleic Acids Res. 18:6445-6445 (1990).
RN [2]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 65-74; 118-127 AND 165-174.

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RC TISSUE=liver;
RX MEDLINE=91354249; PubMed=1883350;
RA Fujita H., Tanaka Y., Noguchi Y., Kono A., Himeno M., Kato K.;
RT "Isolation and sequencing of a cDNA clone encoding rat liver
RT lysosomal cathepsin D and the structure of three forms of mature
RT enzymes.";
RL Biochem. Biophys. Res. Commun. 179:190-196 (1991).
RN [3]
RP SEQUENCE OF 134-170.
RX MEDLINE=89034127; PubMed=3182800;
RA Yonezawa S., Takahashi T., Wang X., Wong R.N.S., Hartsuck J.A.,
RA Tang J.;
RT "Structures at the proteolytic processing region of cathepsin D.";
RL J. Biol. Chem. 263:16504-16511 (1988).
CC -1- FUNCTION: Acid protease active in intracellular protein breakdown.
CC -1- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
CC chain of insulin.
CC -1- SUBUNIT: Occurs as a mixture of both a single chain form and two
CC types of two chain (light and heavy) forms.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: Belongs to peptidase family A1.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X54467; CAA38349.1; -.
DR PIR: S13111; KHRTD.
DR HSSP: P07339; 1LVB.
DR MEROPS: A01.009; -.
DR InterPro: IPR001969; Approtease_AS.
DR InterPro: IPR009007; Pept_A_acid.
DR InterPro: IPR001461; Peptidase_A1.
DR Pfam: PF00026; asp; 1.
DR PRINTS: PR00792; PEPIN.
DR PROSITE: PS00141; ASP_PROTEASE; 2.
KW Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Signal;
KW Lysosome.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 64 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 65 407 CATHEPSIN D.
FT CHAIN 65 164 CATHEPSIN D 12 kDa LIGHT CHAIN.
FT CHAIN 165 407 CATHEPSIN D 30 kDa HEAVY CHAIN.
FT CHAIN 65 117 CATHEPSIN D 9 kDa LIGHT CHAIN.
FT CHAIN 118 407 CATHEPSIN D 34 kDa HEAVY CHAIN.
FT ACT_SITE 97 97 BY SIMILARITY.
FT ACT_SITE 290 290 BY SIMILARITY.
FT DISULFID 91 160 BY SIMILARITY.
FT DISULFID 110 117 BY SIMILARITY.
FT DISULFID 281 285 BY SIMILARITY.
FT DISULFID 324 361 BY SIMILARITY.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 15 15 D -> A (IN REF. 2).
FT CONFLICT 163 163 D -> T (IN REF. 3).
FT CONFLICT 205 205 K -> N (IN REF. 2).
FT CONFLICT 262 262 K -> N (IN REF. 2).
SQ SEQUENCE 407 AA; 44680 MW; C423AD4104D95F84 CRC64;

Query Watch 44.9%; Score 1005; DB 1; Length 407;
Best Local Similarity 48.3%; Pred. No. 1.6e-73;
Matches 196; Conservative 68; Mismatches 124; Indels 18; Gaps 4;

QY 10 LLLLLPLLVNVEGSGATLIRIPHRVQPGRTNLLRGWRE-----PAELPGLGAPSPGD 63
DB 7 LLLLLGLL--DASSSALIRIPLRKFTSIRRTMTVEGGSVEDLILKGPITKYKSMOSSPRTK 64

64 KPFIPLSNRYDVQVFGELGTGTPQNETVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123

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Db 65 EPVSELLKNYLDQAQYIGIGITPPQCFVTVDFTGSSNLWVPSHCKLLDIACVWHKYN 124
Qy 124 PKASSFOAGTCKAIQVGTGRVGDILSED-----KLITGIGKASVIFGEALWPSLV 177
Db 125 SDKSTVTKNGTSDIHGSSLSGLSQTIVSPCKSDLGKIVKQIFGEATKQPGV 184
Qy 178 FAFHFDGILGLGFPILSVEGVRPMPVILVQGLLDKPVFVFLYNRDPPEPDGGLVLGG 237
Db 185 FIAAFDGLGMPFTISVNVKLVFVFDNLKQKLVKFNIFSYLNRDPTGPGGELMLGG 244
Qy 238 SDPAHYTPPLTFVTPVTPAYQIHMVKKVGPGLTCLAKGCAAILDTSITIGTTEIR 297
Db 245 TDSRYXHGELSYLNVTRKAYQVHMDDQVSELTCLCKGCGEALVDTGTSLLVGPVDEVK 304
Qy 298 ALHAAIGIPILAGEYIILCEIPLKPAVSVFLGGVWENLTHDVIVCTTRNGVRLCLSG 357
Db 305 ELQKAIKANVLIQEQYMLPCKEVSLSPLITFKLGGQNVHELPEKIVKVSQAGKTICLSG 364
Qy 358 FQALDVPFPAGPFWILGDFVLTGYVAVFDRGDMKSSARVGLARAT 403
Db 365 FMGMDIPPPSGPLWLGDFVIGCYTYVDR-----EYNRVGFAXAAT 406

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RESULT 7

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CATD MOUSE STANDARD; PRT; 410 AA.
AC P18242;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=91088345; PubMed=2263503;
RA Dietrich J.F., Staekus K.A., Retzel E.F., Haase A.T.;
RT "Nucleotide sequence of a cDNA encoding mouse cathepsin D.";
RL Nucleic Acids Res. 18:7184-7184 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90326544; PubMed=2374732;
RA Grusby M.J., Mitchell S.C., Glimcher L.H.;
RT "Molecular cloning of mouse cathepsin D.";
RL Nucleic Acids Res. 18:4008-4008 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RC MEDLINE=94280622; PubMed=8011168;
RA Hetman M., Perschl A., Saftig P., von Figura K., Peters C.;
RT "Mouse cathepsin D gene: molecular organization, characterization of
the promoter, and chromosomal localization.";
RL DNA Cell Biol. 13:419-427 (1994).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;
RC MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.M., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gin-His-5 bond in B
CC chain of insulin.
CC -!- SUBUNIT: Consists of a light chain and a heavy chain.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- SIMILARITY: Belongs to peptidase family A1.
CC
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CC
CC EMBL; X53337; CAA37423.1; -
CC EMBL; X52886; CAA37067.1; -
CC EMBL; X68378; CAA48453.1; -
CC EMBL; X68379; CAA48453.1; JOINED.
CC EMBL; X68380; CAA48453.1; JOINED.
CC EMBL; X68381; CAA48453.1; JOINED.
CC EMBL; X68382; CAA48453.1; JOINED.
CC EMBL; X68383; CAA48453.1; JOINED.
CC EMBL; BC054758; AAH54758.1; -
CC EMBL; BC057931; AAH57931.1; -
CC PIR; I48278; KMSD.
CC HSP; P07339; ILYB.
CC MEROPS; A01.009; -.
CC MGD; MGI:88562; Ctad.
CC InterPro; IPR001969; Aspartate AS.
CC InterPro; IPR009007; Peptidase Al.
CC InterPro; IPR001461; Peptidase Al.
CC Pfam; PF00026; asp; 1.
CC PRINTS; PR00792; PEPsin.
CC PROSITE; PS00141; ASP_PROTEASE; 2.
CC Hydrolase; Aspartyl protease; Glycoprotein, Lysosome; Zymogen; Signal.
CC SIGNAL 1 20
CC PROFEP 21 64
CC CHAIN 65 410
CC ACT_SITE 97 97
CC ACT_SITE 293 293
CC DISULFID 91 160
CC DISULFID 110 117
CC DISULFID 284 288
CC DISULFID 327 364
CC CARBOHYD 134 134
CC CARBOHYD 261 261
CC SEQUENCE 410 AA; 44954 MW; DC4928EC46928BF0 CRC64;
Query Match 44.3%; Score 992.5; DB 1; Length 410;
Best Local Similarity 47.7%; Pred. No. 1.6e-72;
Matches 194; Conservative 67; Mismatches 125; Indels 21; Gaps 4;
Qy 10 LLALLPLLVPEPGATLIRPLHRVQPGRTLLRGWRE-----PAELPKLGAPSPGD 63
Db 7 LLALLGLL--ASSFAIRIPRLKFRSIRKMTVGSGVEDLILKGPITKYSQSSPKTT 64
Qy 64 KPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFD 123
Db 65 EPVSELLKNYLDQAQYIGIGITPPQCFVTVDFTGSSNLWVPSHCKLLDIACVWHKYN 124
Qy 124 PKASSFOAGTCKAIQVGTGRVGDILSED-----EYNRVGFAXAAT 174

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Db 125 SKSSTVYKNGTSFDIHYGSGSLSGYLSDQTSVSPCKSQSKARGIKVEKQIFGEATKOP 184
QY 175 SLVFAFAHGDGILGFGPILSVGVRPPMDVLVEQGLDKPVFSFYINRDPEEPDGGELV 234
Db 185 GIVEFAAKFDGILGWGYPHISVNNVLPVFDNLMOQKLVKDNIFSFVLNRDPGQPGGELM 244
QY 235 LGGSDPAHYPIPLTFVFTVTPVPAWQHMERVKVGPGLTLCAGCAAILDTGTSITGPTPE 294
Db 245 LGGTSKYHGLSLVNLTRKAYWQHMDQLEGVNELTCKGCEAIVDTGTSLLVGPVE 304
QY 295 EIRALHAALGGIPLLAGELVILLCSEIPKLPVPSFLGQVWFNLTAHDYVVIQTRNGVRLC 354
Db 305 EVKELQKALGAVPLLOGETMPCERKSSVLTPTVLKGGKNYELHPDKYILKVSQGGKTC 364
QY 355 LSGFQALDVPVPPAGPFWILGDVFLGTVAVFDGDMKSSARVGLARA 401
Db 365 LSGFMGMDIPPPSGPLWILGDVFIGSYTVFDR----DNRVGFANA 407

RESULT 8
CATD_BOVIN
ID CATD_BOVIN STANDARD; PRT; 390 AA.
AC P80209; Q9TS27;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN CTSD.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE=1-48.
RC TISSUE=Milk;
RX MEDLINE=93202276; PubMed=8454061;
RA Larsen L.B., Boisen A., Petersen T.E.;
RT "Procatepsin D cannot autoactivate to cathepsin D at acid pH.";
RL FEBS Lett. 319:54-58(1993).
RN [2]
SEQUENCE OF 45-390, AND X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RC TISSUE=Liver;
RX MEDLINE=93223670; PubMed=8467789;
RA Metcalf P., Fusek M.;
RT "Two crystal structures for cathepsin D: the lysosomal targeting
signal and active site.";
RL EMBO J. 12:1293-1302(1993).
CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
chain of insulin.
CC -!- SUBUNIT: Consists of a light chain and a heavy chain.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- SIMILARITY: Belongs to peptidase family A1.
DR HSP; P07339; 1LYB.
DR MEROPS; A01.009; .
DR InterPro; IPR001969; Aspartic protease_AS.
DR InterPro; IPR009007; Pept_A acid.
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen.
FT PROPEP 1 44
FT CHAIN 45 390
FT ACT_SITE 77 77
FT ACT_SITE 273 273
FT DISULFID 71 140
FT DISULFID 90 97
FT DISULFID 264 268
FT DISULFID 307 344
FT CARBOHYD 114 114
N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 390 AA; 42488 MW; 5B38AA1C33C48D35 CRC64;
Query Match 43.2%; Score 967.5; DB 1; Length 390;
Best Local Similarity 48.3%; Pred. No. 1.6e-70;
Matches 189; Conservative 58; Mismatches 125; Indels 19; Gaps 3;
QY 26 LIRPLHRVQPORRLNLRGW-----REPAELPKLGAPSGDKPIFVPLSNYRDVOVF 79
Db 1 VIRIPLHKFTSIRRTMSEAAGXVXXLIAKGPISKVATGEPAVRQGPPELLKXNDAYY 60
QY 80 GEIGLTGPQNPNTVAFTDGSSNLWVPSSRRCHFFSVPCWMLHHRFDPKSSSQANSTKPAI 139
Db 61 GEIGLTGPQCPQTVVFDTGSAANLWVPSIHCILLDIACWTKRKYNSDKSSTVYKNGTTEDI 120
QY 140 OYGTGRVDGILSSEDKLTI-----GKINGASVFGEALWEPSLVFAFAHGDGILG 190
Db 121 HYGSGSLGYLSQDTSVPCNPSSPGVTVQRTFGEARLQKGVVFIKAFHGDGILGMA 180
QY 191 FPILSVEGVRPPMDVLVEQGLDKPVFSFYINRDPEEPDGGELVGGSDPAHYPIPLTFV 250
Db 181 YPRISVNNVLPVFDNLMOQKLVKDNVFSFELNRDPKAPGGELMLGGTDSKYIRGSLMFH 240
QY 251 PTVTPAYWQHMERVKVGPGLTLCAGCAAILDTGTSITGPTPEIRALHAALGIPILA 310
Db 241 NVTRQAYWQHMDQLDVGSSLTVCCKGCEAIVDTGTSILVGPVEVRELOKAGVPLIQ 300
QY 311 GEYIILCSEIPKLPVPSFLGQVWFNLTAHDYVVIQTRNGVRLCLSGFQALDVPVPPAGPF 370
Db 301 GEYMIPECRKSLSPEVTVLKGGKDYALSPEDYALKVSOAETTVCLSGFMGMDIPPPGGPL 360
QY 371 WILGDVFLGTVAVFDGDMKSSARVGLARA 401
Db 361 WILGDVFIGRYTVFDR----DQNRVGLAEA 387

RESULT 9
ASPP_AEDAE
ID ASPP_AEDAE STANDARD; PRT; 387 AA.
AC Q03168;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysosomal aspartic protease precursor (EC 3.4.23.-).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 54-71.
RP MEDLINE=93016141; PubMed=1400492;
RX Cho W.L., Raikhel A.S.;
RT "Cloning of cDNA for mosquito lysosomal aspartic protease. Sequence
analysis of an insect lysosomal enzyme similar to cathepsins D and
E.";
RL J. Biol. Chem. 267:21823-21829(1992).
RN [2]
CHARACTERIZATION.
RP Cho W.-L., Dhadialla T.S., Raikhel A.S.;
RT "Purification and characterization of a lysosomal aspartic protease
with cathepsin D activity from the mosquito.";
RL Insect Biochem. 21:165-176(1991).
CC -!- FUNCTION: May degrade organelles involved in the biosynthesis and
secretion of vitellogenin.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- SIMILARITY: Belongs to peptidase family A1.
CC
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CC EMIL; M95187; AAA29350.1; -.
CC PIR; A45117; A45117.
DR HSP; P00797; 2REN.
DR MEROPS; A01.009; -.
DR Siena-2DPAGE; Q03168; -.
DR InterPro; IPR001969; Aspartic protease AS.
DR InterPro; IPR009007; Pept A acid_
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; asp; 1.
DR PRINTS; P00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 18
FT PROPEP 19 53
FT CHAIN 54 387
FT ACT_SITE 86 86
FT ACT_SITE 272 272
FT DISULFID 99 106
FT DISULFID 263 267
FT DISULFID 306 343
FT CARBOHYD 123 123
SQ SEQUENCE 387 AA; 41805 MW; 73A3C9E701E47EEC CRC64;

Query Match 43.1%; Score 964.5; DB 1; Length 387;
Best Local Similarity 48.5%; Pred. No. 2.8e-70;
Matches 192; Conservative 62; Mismatches 131; Indels 11; Gaps 5;

QY 6 LQPELLLLPLNVEPGATLIRPLHVRQGRRTNLLRGWRBFAELPKLGAPSPGDKP 65
D 1 LIKSHIALVCLAVL--SOADFRVQLHKTESARQHFRNVDTIKQLRL-KYNAYS--GP 55
QY 66 IFVPLSNRVDQYGEIGLGPONFTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDP 125
D 56 VPEPLSNYLDQYGAITGTPPOSKVFDGSSNLWVPSKCSFTNACIMENKYNK 115
QY 126 ASSSFQANGTKFAIQYGTGRVDGILSDKLIGIKGASVIFGEALWPSLVFAFAFDG 185
D 116 KSTTFERKGAFAHQYSGSLSGVLTDTVGLGGVSVTKQTFABAINPGLVFAAFDG 175
QY 186 ILGLGFPILSVGVRPMDVULVEQGLDKVPFYLNRDPPEPGGELVGLGSPAHYIP 245
D 176 ILGLGYSSISVDGVVPVFNMFNGLIDAPVFSYLNRPDPAEAGEGIIFGSDSNKYTG 235
QY 246 PLTFVPTVTPVMOIHMERVKVFGTLTI-CAKGCRAILDTGSLITGTEIRALHAIGG 305
D 236 DFTVLSVDRKAYWQFMDSVKVG-DTEFCNNGCEALADTGLSLIAGPVSEVTAINKAIGG 294
QY 306 IPLLAGEYIILCSBIPKLPAPVSLFGVWVFNLTADHYVVIQTRNGVRILCLSGFQALDVP 365
D 295 TPIMNGEYVMDCSLIPKLPKISFVLGKGSFDEGADYVLRVAQNGKICLSGFMDIIPP 354
QY 366 PAGPFWILGDVFLTYVAVDRGMDKMSARVGLARA 401
D 355 PNGPLWILGDVFIKYYTEFDMG----NDRVGFATA 386

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RESULT 10
CATD_PIG
ID CATD_PIG STANDARD; PRT; 345 AA.
AC P00795;
DT 21-JUL-1996 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin D (EC 3.4.23.5).
GN CTSD.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

```

RP SEQUENCE OF 1-98.
RC TISSUE=Spleen;
RX MEDLINE=83213348; PubMed=6406481;
RA Takahashi T., Tang J.;
RT "Am.no acid sequence of porcine cathepsin D light chain.";
RL J. Biol. Chem. 258:6435-6443(1983).
RN [2]
RP SEQUENCE OF 104-345.
RC TISSUE=Spleen;
RX MEDLINE=84222027; PubMed=6587385;
RA Shewale J.G., Tang J.;
RT "Am.no acid sequence of porcine spleen cathepsin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3703-3707(1984).
RN [3]
RP SEQUENCE OF 74-148 FROM N.A.
RX MEDLINE=89034127; PubMed=3182800;
RA Yonezawa S., Takahashi T., Wang X., Wong R.N.S., Hartsuck J.A.,
RT "Structures at the proteolytic processing region of cathepsin D.";
RL J. Biol. Chem. 263:16504-16511(1988).
RN [4]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=94152787; PubMed=642853;
RA Nakao Y., Kozutsumi Y., Kawasaki T., Yamashina I., van Halbeek H.,
RT Vliegenthart J.F.G.;
RL "Oligosaccharides on cathepsin D from porcine spleen.";
RT Arch. Biochem. Biophys. 229:43-54(1984).
CC -1- FUNCTION: Acid protease active in intracellular protein breakdown.
CC -1- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-His-5 bond in B
CC chain of insulin.
CC -1- SUBUNIT: Consists of a light chain and a heavy chain.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: Belongs to peptidase family A1.
DR HSP; P07339; ILYB.
DR MEROPS; A01.009; -.
DR InterPro; IPR001969; Aspartic protease AS.
DR InterPro; IPR009007; Pept A acid_
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; asp; 1.
DR PRINTS; P00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydroxylase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen.
FT CHAIN 1 98
FT CATHEPSIN D LIGHT CHAIN.
FT CHAIN 104 345
FT ACT_SITE 33 33
FT ACT_SITE 230 230
FT DISULFID 46 53
FT DISULFID 221 225
FT DISULFID 264 301
FT CARBOHYD 70 70
FT CARBOHYD 198 198
FT VARIANT 234 234
FT VARIANT 247 247
FT CONFLICT 89 89
FT CONFLICT 97 97
SQ SEQUENCE 345 AA; 37295 MW; B3E72C11787F14E2 CRC64;

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Query Match 42.2%; Score 944; DB 1; Length 345;
Best Local Similarity 52.7%; Pred. No. 1.1e-68;
Matches 183; Conservative 48; Mismatches 102; Indels 14; Gaps 4;
QY 65 PIFVPLSNRVDQYFGEIGLGTTPQNTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDP 124
D 2 PIFVPLSNRVDQYFGEIGLGTTPQNTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDP 124
QY 125 KASSSFQANGTKFAIQYGTGRVDGIL-SEDKL-----ICGKASVIFGEALWEP 174
D 62 GKSTTVKNGTTFAIHYGSGSLSGVLTDTVGLGGVSVTKQTFABAINPGLVFAAFDG 294
QY 175 SILVFAFAHFDGILGLGFPILSVGVRPMDVULVEQGLDKVPFYLNRDPPEPGGELV 234
D 122 GLTFIAAKFDGILGMAYPRISVNNVVFDFNLQKLVKDFISFYLNRDPGAPGQGLM 181


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Qy 235 LGSDDPAHYIPPLTFVPTVYVQVHMERVKVGPGLTCAKGCALDVTGTSITLTGTE 294
Db 182 LGGIDSKYKSGSLDHYHNRKAYQVHMERVAVGSSLTLCRGCEAIVDTGTSITLVQPE 241
Qy 295 EIRALHAAGIPILLAGEYIILCSIEPKLPAVSLGGLGWENLTAHDVVIOTTRNGVRLC 354
Db 242 EVRELKALGAVPLIQEYMLPCEKVPSPDVTYTLGGKKYKLSSENLYLKVSAQGQTIC 301
Qy 355 LSGFQALDVPVPPAGFWLGVDFVIGTVYVAFDRGDMKSSARVGLARA 401
Db 302 LSGFMGMDIPPPGGFLMGDFVIGRYTYTFDR-DLN---RVGLAEA 344

RESULT 11
CATD SHEEP
ID CATD SHEEP STANDARD; PRT; 365 AA.
AC Q9MZS8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5) (fragment).
GN CTSD.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN 1
RP SEQUENCE FROM N.A., AND VARIANT CONCL ASN-268.
RC STRAIN=White Swedish Landrace;
RX MEDLIN=20315962; PubMed=10856224;
RA Tyndela J., Sohar I., Sleat D.E., Gin R.M., Donnelly R.J., Baumann M.,
RA Halcia M., Lobel P.;
RT "A mutation in the ovine cathepsin D gene causes a congenital
RT lysosomal storage disease with profound neurodegeneration.";
RL EMBO J. 19:2786-2792(2000).
CC -!- FUNCTION: Cathepsin D is an acid protease active in intracellular
CC protein breakdown.
CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
CC chain of insulin.
CC -!- SUBUNIT: Occurs as a mixture of both a single chain form and two
CC types of two chain (light and heavy) forms (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- DISEASE: Defects in CTSD are a cause of congenital ovine neuronal
CC ceroid lipofuscinosis (CONCL). CONCL is an autosomal recessive
CC disorder. Newborn lambs are weak, trembling, and unable to rise
CC and support their bodies. However, they are able to vocalize,
CC support their heads, and to suckle if bottle-fed. At autopsy, the
CC brains of affected lambs are strikingly small. The deep layers of
CC the cerebral cortex show pronounced neuronal loss, reactive
CC astrocytosis, and infiltration of macrophages. There is severe
CC degeneration of hippocampal pyramidal neurons.
CC -!- SIMILARITY: Belongs to peptidase family A1.
CC
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CC
CC EMBL; AF164143; AAF80494.1; -.
CC HSSP; P07339; 1LYB.
CC MEROPS; A01.009; -.
CC InterPro; IPR001969; Asparticase AS.
CC InterPro; IPR009007; Pept_A Acid.
CC InterPro; IPR001461; Peptidase_A1.
CC Pfam; PF00026; asp; 1.
CC PRINTS; PR00792; PEPSIN.
CC PROSITE; PS00141; ASP_PROTEASE; 2.

Hydrolase; Aspartyl protease; Glycoprotein; Zymogen;
Lysosome; Disease mut.
FT NON_TER 1
FT PROFEP <1 39 ACTIVATION PEPTIDE.
FT CHAIN 40 >365 CATHEPSIN D.
FT ACT_SITE 72 72 BY SIMILARITY.
FT ACT_SITE 268 268 BY SIMILARITY.
FT DISULFID 66 135 BY SIMILARITY.
FT DISULFID 85 92 BY SIMILARITY.
FT DISULFID 259 263 BY SIMILARITY.
FT DISULFID 302 339 BY SIMILARITY.
FT VARIANT 268 268 D -> N (IN CONCL; INACTIVE).
FT NON_TER 365
SQ SEQUENCE 365 AA; 39814 MW; 76A7BF5BC45E9CB CRC64;

Query Match 41.2%; Score 922.5; DB 1; Length 365;
Best Local Similarity 47.7%; Pred. No. 6.2e-67;
Matches 175; Conservative 61; Mismatches 110; Indels 21; Gaps 4;

Qy 31 LHRVQGRRTLNLLRGWREPAE-----LPKLGAPSGDK--PIFVLSNYRDVQYFGE 81
Db 1 LHKFTSNRRRTMSEAWG---PVEHLIAKGPISKYATREPAPVQGPPELNTYMDAQYIGE 57
Qy 82 IGLGTPQNFVAFDTGSSNLWVPSRRCHFFSPVCLHHRDPDKASSFQANGTKPAIQY 141
Db 58 IGIETPPQCFVWFDTGSANLWVPSIHCKLDIACVHVKYNSDKSSTYVKNGTTFDIHY 117
Qy 142 GTGRVDGLTSEDKLT-----GGIKGASVIFGEALWEPSSLVFAFAHFDGILGLGFP 192
Db 118 GSGSLGYLSQDTVSPCNPSSSPGVTVQRTFGEAIGKQGVFFIAKEDGILGNAYP 177
Qy 193 ILSVEGVRRPPMDVLVEQGLDLPVFSFYLNRRDPPEPDGSELVLGGSDPAHYIPPLTFVY 252
Db 178 RISVNNVLPVDNLMRQKLVKDNVFSFLNRPDKAQPGSELMLG3TDSKYRGSILTYHN 237
Qy 253 TVPAWQVHMERVKVGPGLTCAKGCALDVTGTSITLTGTPTEIRALHAAGIPLAGE 312
Db 238 TRQAWQVHMDQLDVGSSLTVCCKGCEAIVDTGTSILAVGPVDVREHLKAGAVPLIQE 297
Qy 313 YILCSIEPKLPAVSLGGLGWENLTAHDVVIOTTRNGVRLC SGFQALDVPVPPAGPWI 372
Db 298 YNIPCEKVSSLPQVTLKLGKDYTLSPEDYTLKVSQAGTTVCLSGFPMGMDIPPPGGPLMI 357
Qy 373 LGDVFGL 379
Db 358 LGDVFIG 364

RESULT 12
CATD MOUSE
ID CATD MOUSE STANDARD; PRT; 397 AA.
AC P70269; O35647;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cathepsin E precursor (EC 3.4.23.34).
GN CTSE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Spleen;
RX MEDLINE=97324100; PubMed=9180269;
RA Tatnell P.J., Lees W.E., Kay J.;
RT "Cloning, expression and characterisation of murine procathepsin E.";
RL FEBS Lett. 408:62-66(1997).
RN 2
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Tatnell P.J., Roth W., Duesing J., Kay J., Peters C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
```


Db 364 PFAGPLWILGDFVIRKFXSVFDRG-----NNQVG LAPA 396

RESULT 15
CATE RABIT STANDARD; PRT; 396 AA.
ID CATE_RABIT STANDARD; PRT; 396 AA.

ID	CATE_RABIT	STANDARD;
AC	P43159;	
DT	01-NOV-1995 (Rel. 32, Created)	
DT	01-NOV-1995 (Rel. 32, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Cathepsin E precursor (EC 3.4.23.34).	
GN	CTSE..	
OS	Oryctolagus cuniculus (Rabbit).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
NBI	NCBI_TaxID=9986;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Japanese white;	
RX	MEDLINE=94009032; PubMed=8404890;	
RA	Kagayama T.;	
RT	"Rabbit cathepsain E and cathepsin F. Nucleotide sequence of cDNA,	
RT	hydrolytic specificity for biologically active peptides and gene	
RL	expression during development.";	
RL	Eur. J. Biochem. 216:717-728(1993).	
-!	FUNCTION: Due ot its intracellular location and distribution in	
CC	lymphoid associated tissue, it may have a role in immune function.	
CC	-! CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader	
CC	specificity.	
CC	-! SUBUNIT: Homodimer; disulfide-linked (By similarity).	
CC	-! SIMLARTY: Belongs to peptidase family A1.	
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CC	or send an email to licensel@isb-sib.ch).	
EMBL:	L08418; AAC37308.1; -.	
PIR:	S36865; S36865.	
HSSP:	P00794; 4CMS.	
MEROPS:	A01.010; -.	
InterPro:	IPR001969; Aspartate AS.	
InterPro:	IPR009007; Peptide acid_	
InterPro:	IPR001461; Peptidase_A1.	
Pfam:	PF00026; asp; 1.	
PRINTS:	PR00792; PEPSIN.	
DROME:	PS00141; ASP PROTEASE; 1.	
KW	Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal;	
KM	Pyroglutamate carboxylic acid.	
FT SIGNAL	1 17 POTENTIAL.	
FT PROPEP	18 53 ACTIVATION PEPTIDE (BY SIMILARITY).	
FT CHAIN	54 396 CATHEPSIN E.	
FT MOD_RES	18 18 PYROGLUTAMINE CARBOXYLIC ACID	
FT ACT_SITE	96 96 (BY SIMILARITY).	
FT ACT_SITE	281 281 BY SIMILARITY.	
FT DISULFID	60 60 INTERCHAIN (PROBABLE) .	
FT DISULFID	109 114 BY SIMILARITY.	
FT DISULFID	272 276 BY SIMILARITY.	
FT DISULFID	314 351 BY SIMILARITY.	
FT SEQUENCE	396 AA; 42679 MW; E5D84FE48DC760AA CRC64;	

Query Match 37.9%; Score 848.5; DB 1; Length 396;
Best Local Similarity 44.9%; Pred. No. 6.2e-61;
Matches 179; Conservative 68; Mismatches 137; Indels 15; Gaps 7;

Oy 9 PLLLLLLPLLNVFPSCATLRIPDLHRVQCGRPTNLIRG-----WR-EPAELPKLGAPSPG 62
||||| : :: | | : || : | | : | : :
5 PLLLLL-LIIDLQAQGTLDRVPILRR-QFSLRKKLAQQGSLEFWKAHKVDVMQYTETCTM 62

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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:14:10 ; Search time 28.59 Seconds
(without alignments)
1413.099 Million cell updates/sec

Title: US-09-700-770-8
Perfect score: 2238
Sequence: 1 MSPPPHLLQPLLLPLLNVE.....ARTRGADLWGETAQAQPPG 420

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1030	46.0	398	2	I51185
2	1015	45.4	412	1	KHHUD
3	1005	44.9	407	1	KHRTD
4	922.5	44.3	410	1	KHMSD
5	964.5	43.1	387	2	A45117
6	954.5	42.6	344	1	KHPGD
7	905.5	40.5	444	2	T24204
8	869	38.8	396	2	A34401
9	867	38.7	398	2	S66465
10	848.5	37.9	396	2	S36885
11	830	37.1	508	2	S19697
12	808.5	36.1	401	1	RMSS
13	806.5	36.0	391	2	A43356
14	804	35.9	509	2	S66516
15	803.5	35.9	442	2	UC5077
16	797	35.6	402	1	RMSK
17	789.5	35.3	365	2	S66466
18	783	35.0	400	2	I47099
19	779	34.8	402	1	RERTK
20	779	34.8	406	1	REHUK
21	778.5	34.8	474	2	T12049
22	778	34.8	513	2	T11686
23	774	34.6	506	2	T07915
24	774	34.6	508	2	D85056
25	773.5	34.6	496	2	U09732
26	769.5	34.4	513	2	T09739
27	767.5	34.3	388	1	S19682
28	766.5	34.2	506	2	F86293
29	765.5	34.2	388	1	PEMQAR

30	765.5	34.2	509	2	JC7272
31	765	34.2	506	2	S71591
32	760.5	34.0	428	2	S47096
33	759.5	33.9	388	1	PEHU
34	757.5	33.8	388	1	S19684
35	757.5	33.8	388	2	B30142
36	756	33.8	398	2	T33383
37	755.5	33.8	388	1	PEMQAR
38	754.5	33.7	388	2	A30142
39	754	33.7	509	2	S49349
40	737	32.9	387	2	C38302
41	735.5	32.9	386	1	PEPG
42	733	32.8	387	2	D38302
43	717	32.0	385	2	JC7575
44	717	32.0	387	2	B38302
45	707.5	31.6	383	2	A41443

ALIGNMENTS

RESULT 1

I51185
cathepsin D (EC 3.4.23.5) precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 22-Jun-1999
C:Accession: I51185
R:Retzek, H.; Steyrer, E.; Sanders, E.J.; Nimpf, J.; Schneider, W.J.
DNA Cell Biol. 11, 661-672, 1992
A:Title: Molecular cloning and functional characterization of chicken cathepsin D, a
A:Reference number: I51185; MUID:93039672; PMID:1418623
A:Accession: I51185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-398 <RET>
A:Cross-references: GB:S49650; NID:g259834; PIDN:AAB24157.1; PID:g259835
C:Superfamily: pepsin
C:Keywords: aspartic proteinase; hydrolase

Query Match 46.0%; Score 1030; DB 2; Length 398;
Best Local Similarity 50.0%; Pred. No. 3.6e-78;
Matches 208; Conservative 57; Mismatches 115; Indels 36; Gaps 7;

Qy	1	MSPPPHLLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRITLNLGRWREPAELPKLGA--	58
Db	1	MAPRGLL--VLLLLAL--VGPC-AALIRIPLTSTTRMLT-----EVGEIPDMNAIT	50
Qy	59	-----PSPGDKPIFVPLSNYRDVQYFGEIGLGTTPQNFVAFDTGSSNLWV	104
Db	51	QLKFKLGFADLAEP--BILKNYMDAQYGEIGTTPQKFTVWVDTGSSNLWV	104
Qy	105	PSRCHFPSPVCMHHRFDPKASSFOANGTKPAIQVGTGRVDGILSEDKLTIGGIGKAS	164
Db	105	PSVCHLLDACLHKKYDASKSTYVENGTETFAIHYGTSGLSGLSQDTVTLLNLKKN	164
Qy	165	VIFGEALWPSLWFAFAHFGIILGFPILSVGEVRPPMDVLEQGLDKPVPFYLNRD	224
Db	165	QIFGEAVKQGIPIAAKFGILLGMAPRISVDKVTFFDNVMOQKLEKNIFSFLNRD	224
Qy	225	PEPDGDELVLGSDPAHYIPPLTFVPTVPAVQIHMVRKVGPGLTLCAGCAAILDT	284
Db	225	PTAQGGELLGGTDPKYSGDFSWNVTRKAYQVHMSVDVANGLTLCCKGCEALVDT	284
Qy	285	GTSLITGPTTEIRALHAIGIIPLLAGEYIILSEIKPLPAVFLGGVFNLTAAHYVI	344
Db	285	GTSLITGPTKEVKELOTAIGAKPLIKQYVISCDSLSFLVTLMLGKPYQLTGEQYVF	344
Qy	345	QTTTANGVRLCLSGFOALDVPVPPAGPFWILGDFVLTGVVAVFDGDMKSSARVGLAR	400
Db	345	KVSAQGETICLSGFGSLDVPVPPGGLWILGDVFIIGVPIYTVFDR-----DNDSVGVFAK	396

RESULT 2

C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degrada
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-64/Domain: propeptide #status predicted <PRO>
F;65-162,169-410/Product: cathepsin D #status experimental <MAT>
F;267,329-356/Region: phosphotransferase recognition
F;91-160,110-117,286-290,329-366/Diulfide bonds: #status experimental
P;97,295/Active site: Asp #status experimental
P;134,263/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 45.4%; Score 1015; DB 1; Length 412;
Best Local Similarity 46.9%; Pred. No. 6.7e-77;
Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

QY 1 MSPPELLQLLLLEPLLNVSPSGATLRIPLHRVQPGRRTNLILRGWRE-----PAELP 54
DB 1 MQPSLLPLALCLL----AAPASA-LVRIPLHKETSLRRTWSEVGGSVEDLIAKGPYSKY 55

QY 55 KLGAPEGDKPIFVPLSNRYRDVOYFGHGLGTTPQNFTVPADTGSSNMLWPESRRCHFFSV 114
DB : ::
DB 56 SQAVPAVTGEPIPELVKNYMDAQQYGGIGTGPQCFTTVDFDTGSSNMLWVPSIHKCLADI 115

QY 115 PCWLHHRFDPKASSFQANGTKAIQYCTGRVDGIILSEDKLTI-----GGIKGA 163
DB : ::
DB 116 ACMIHHKSDKSTYYVNGTGFSDIHVYGSSLSYLSDQTIVSVCQSASSASALGGVKVE 175

QY 164 SVIFGEALWEPSLVAFAPHAHDGIIILGFPFILSVSGVRPPMDVLVEQQILLDPVFVSFYLNLR 223
DB : ::
DB 176 RQVFGREATQGKITFAAKFDGILGMAYPRISVNVLVPFDNLMQOKLVQDNIFSFLSR 235

QY 224 DPKEPDGDELVLGSSDPAHYIPBLTFVPTVPAYWQJHMERVKYKPGTLTCAKGAAAILD 283
DB : ::
DB 236 DPDAQPGEGEMLGGTDUSKKYKGSLSYLVNRKAYWQHLDQVEVASGTLCKEGCEATVD 295

QY 284 TGTSLTGTPTEERIALHAAICGGLLAGEVYILCSEIPKLPVASFLLGGVWFNLTAHDYV 343
DB : ::
DB 296 TGTSLWGVFVDVRELQKALGAPLIQGYMPCVKYSTLPAILTLGGKGYKLSPEYDT 355

QY 344 IQTRNGVRLCSLGFAQDLVPPAGPFMWILDVFLGTGYVAVDFRDMKMSARVGLARA 401
::
DB 356 LKVSQAQKTCLSGFMGMIDPPSPGPLWILGDVFIEGYTYTVFDR---DNNRVGFAEA 409

RESULT 3
KHRTD
cathepsin D (EC 3.4.23.5) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 18-Jun-1999
C;Accession: S13111; C31918; JQ1177; PQ0222
R;Birch, N.P.; Loh, Y.P.
Nucleic Acids Res. 18, 6445-6446, 1990
A;Title: Cloning, sequence and expression of rat cathepsin D.
A;Reference number: S13111; MUID:91057150; PMID:2243802
A;Accession: S13111
A;Molecule type: mRNA
A;Residues: 1-407 <BIR>
A;Cross-references: EMBL:X5A467; NID:g55881; PIDN:CAA38349, 1; PID:g55882
R;Yonewawa, S.; Takahashi, T.; Wang, X.; Wong, R.N.S.; Hartsuck, J.A.; Tang, J.
J. Biol. Chem. 263, 16504-16511, 1988
A;Title: Structures at the proteolytic processing region of cathepsin D.
A;Reference number: A92681; MUID:89034127; PMID:3182800
A;Accession: C31918
A;Molecule type: Protein
A;Residues: 134-162, V', 164-170 <YON>
R;Fujiita, H.; Tanaka, Y.; Noguchi, Y.; Kono, A.; Himeno, M.; Kato, K.
Biochem. Biophys. Res. Commun. 179, 190-196, 1991
A;Title: Isolation and sequencing of a cDNA clone encoding rat liver lysosomal cathepsin D.
A;Reference number: JQ1177; MUID:91354249; PMID:1883350
A;Accession: JQ1177
A;Molecule type: mRNA
A;Residues: 1-14, A', 16-204, 'N', 206-261, 'N', 263-407 <FUJ>
A;Accession: PQ0222
A;Molecule type: Protein
A;Residues: 65-74; 118-127; 165-174 <FU2>

A;Cross-references: EMBL:X53337; NID:g50300; PIDN:CAA37423.1; PID:g50301
R;Grusby, M.J.; Mitchell, S.C.; Glimcher, L.H.
Nucleic Acids Res. 18, 4008, 1990
A;Title: Molecular cloning of mouse cathepsin D.
A;Reference number: S12587; MUID:90326544; PMID:2374732
A;Accession: S12587
A;Molecule type: mRNA
A;Residues: 1-410 <GRU>
A;Cross-references: EMBL:X52886; NID:g50298; PIDN:CAA37067.1; PID:g50299
C;Genetics:
A;Introns: 23/2; 76/3; 118/1; 157/3; 233/2; 274/2; 322/3; 355/3
C;Function:
A;Description: limited specificity endopeptidase
A;Pathway: intracellular protein degradation
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-64/Domain: propeptide #status predicted <PRO>
F;65-410/Product: cathepsin D, single-chain form #status predicted <MAT>
F;91-160,110-117,284-288,327-364/Disulfide bonds: #status predicted
F;97,293/Active site: Asp #status predicted
F;134,26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.3%; Score 992.5; DB 1; Length 410;
Best Local Similarity 47.7%; Pred. No. 5e-75;
Matches 194; Conservative 67; Mismatches 125; Indels 21; Gaps 4;

QY 10 LLLLLLLNVPSPGATLIRPLHRVQGRPTNLRLGWR-----PAELPKLGAPSPGD 63
DB 7 LLLILGLL--ASSSFAIRIPLRKFTSIRRTMTVEGGSVEDLILKGPITKYSMOSSPKTT 64
QY 64 KPIFVPLSNRYDQVYFGEIGLGTTPQNFVAFTDGSNNLWVPSRRCHFFSPVCLWHRFD 123
DB 65 EPVSELLKNYLDQAQYGDIGLGTTPQCFVTFDGSNNLWVPSIHCKLIDACWVHKYN 124
QY 124 PKASSSFQANGTFAIYQYGRVDGILSEDKLTI-----GGIKGASVIFGALWEP 174
DB 125 SDKSSTVYVKNQTSPIHIVGSGSLSGYLSQDTSVPCKSDQSKARGIKVEKQIFGEATKQP 184
QY 175 SLVFAFAHFQDGLLGLGPILLVSEGVRRPMDVLVEQGLLDKPVFSFYLNRRDEPDGGELV 234
DB 185 GIVFVAAKFDGILGMVPHISVNNVLVPFDNLMQOKLVDRKNIFSYFLNRDPGPGGSELM 244
QY 235 LGGSDPAHYTPPLTFVPTVPAYVQIEMERVKVGFGLTCAKGAAILDTGTSITGTE 294
DB 245 LGGTDSKYIHGELSYLNVTWKAYQVEMDQLEVNGEITLCKGGCEAIVDTGTSLLVGPE 304
QY 295 EIRALHAAIGGIPILAGEYIILCSEIPKLPAVSFLTGGWENLTAHDYVIOITRNGVRLC 354
DB 305 EVKELQKAI GA VPLIQEYMIPECKVS LPTVYLKGGKNYELHPDKYILKVSOGGKTC 364
QY 355 LSGFQALDVPVPAGPFWILGDVFLGTIVAVPDRGDMKSSARVGLARA 401
DB 365 LSGFMGMGDIPPPSGFLWILGDVFI GSYTYTFDR----DNNRVGFANA 407

RESULT 5
A45117
aspartic proteinase (EC 3.4.23.-), lysosomal - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999
C;Accession: A45117
R;Cho, W.L.; Raikhel, A.S.
J. Biol. Chem. 267, 21823-21829, 1992
A;Title: Cloning of cDNA for mosquito lysosomal aspartic protease. Sequence analysis
A;Reference number: A45117; MUID:93016141; PMID:1400492
A;Accession: A45117
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-387 <CHO>
A;Cross-references: GB:M95187; NID:g293229; PIDN:AAA29350.1; PID:g293230
A;Experimental source: fat body
A;Note: sequence extracted from NCBI backbone (NCBIN:116753, NCBIIP:116754)

QY 250 VPVTPAYWQHMERVKVGLTLCAKCAAILDTGTSITGTEETRALHAAIGIPLL 309
 Db 266 VPVTRKGYWQFMDKV-VGSGVLCGNGCCAIADTGTSLIAGPKAQIEAIONFIEGAEPLI 324
 QY 310 AGEYIILCEIPKLPVAVSFLGGVWFLNTHDYVIOFTRNGVRLCUGSGFOALDVPPPPAG 369
 Db 325 KGEYMSICDQVPTLPVSVFVIGQEFSLKGEDYVVKVSGGKTKICLSGFMGIDLPBRVGE 384
 QY 370 FMIIGDVELCTYVAVEDRGDMKKSARVGLARAT 403
 Db 385 LWILGDVFIKRYYSVFD----FDQNRVGFQAQAKT 414

RESULT 8
 A34401
 cathepsin E (EC 3.4.23.34) precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Jun-1990 #sequence revision 22-Jun-1990 #text_change 22-Jun-1999
 C/Accession: A42038; A34401; S35663; S34467; A34643; B34643
 R/Azuma, T.; Liu, W.; Vander Laan, D.J.; Bowcock, A.M.; Taggart, R.T.
 J. Biol. Chem. 267, 1609-1614, 1992
 A/Title: Human gastric cathepsin E gene. Multiple transcripts result from alternative po
 A/Reference number: A42038; MUID:92112877; PMID:1370478
 A/Accession: A42038
 A/Molecule type: DNA
 A/Residues: 1-396 <AZU>
 A/Cross-references: GB:M84424; GB:M82847; NID:g181203; PIDN:AAA52300.1; PID:g181205
 A/Note: sequence extracted from NCBI backbone (NCBIN:75963, NCBIN:75966, NCBIN:75971, NC
 R/Azuma, T.; Pale, G.; Mohandas, T.K.; Couvreur, J.M.; Taggart, R.T.
 J. Biol. Chem. 264, 16748-16753, 1989
 A/Title: Human gastric cathepsin E. Predicted sequence localization to chromosome 1, and
 A/Reference number: A34401; MUID:89380302; PMID:2674141
 A/Accession: A34401
 A/Molecule type: mRNA
 A/Residues: 1-396 <AZ2>
 A/Cross-references: GB:J05036; NID:g181193; PIDN:AAA52130.1; PID:g181194
 R/Takeda-Ezaki, M.; Yamamoto, K.
 Arch. Biochem. Biophys. 304, 352-358, 1993
 A/Title: Isolation and biochemical characterization of procathepsin E from human erythro
 A/Reference number: S35663; MUID:93349047; PMID:8346912
 A/Accession: S35663
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 20-38;54-76 <TAK>
 R/Hill, J.; Montgomery, D.S.; Kay, J.
 FEBS Lett. 326, 101-104, 1993
 A/Title: Human cathepsin E produced in E. coli.
 A/Reference number: S34467; MUID:93314762; PMID:8325357
 A/Accession: S34467
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 57-60;62-81 <HIL>
 R/Achanda, S.B.P.; Matsuzaki, O.; Kageyama, T.; Takahashi, K.
 Biochem. Biophys. Res. Commun. 168, 878-885, 1990
 A/Title: Structural evidence for two isozymic forms and the carbohydrate attachment site
 A/Reference number: A34643; MUID:90241267; PMID:2334440
 A/Accession: A34643
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 54-58,'XXX',62-64,'M',66-89,'X',91-95 <ATH>
 A/Accession: B34643
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 54-59,'X',61-68 <AT2>
 C/Genetics:
 A/Gene: GDB:CTSE
 A/Cross-references: GDB:119821; OMIM:116890
 A/Map position: 1q31-1q31
 C/Superfamily: pepsin
 C/Keywords: aspartic proteinase; blocked amino end; hydrolase; zymogen
 F/1-17/Domain: signal sequence #status predicted <SIG>
 F/18-53/Domain: activation peptide #status predicted <PRO>
 F/54-396/Product: cathepsin E #status predicted <MAT>

F/18/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone ca
 F;96,281/Active site: Asp #status predicted

Query Match 38.8%; Score 869; DB 2; Length 396;
 Best Local Similarity 45.1%; Pred. No. 9.6e-65;
 Matches 179; Conservative 70; Mismatches 136; Indels 12; Gaps 5;

QY 10 LLLLLLPLNVEPSGATLIRIPHRVQGRRTL----NLLRGWR-EPAELPKLGAPSPGDK 64
 Db 5 LLLLLLLELGEAQGSLHRVPLRRHPSLKKLARSQSLSEFWKSHNLDIMTQTESCMDQ 64
 QY 65 PIFVPLSNYRDVQYFGEIGLGTTPQNTFVADTGTSSNLNWPVSRCHFFSVPCWLHHRFDP 124
 Db 65 SAKERLINYLDMEYFGTISIGSPQNTFVIFDTGSSNLNWPVSVYC--TSPACKTHRFQF 122
 QY 125 KASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKAGSVIFGEALWEPVSLVFAFHD 184
 Db 123 SQSSTYSQSQSFSIQYGTGSLSGIIGADQVSVEGTVVQQQGEVSVEPQCFVDAEFD 182
 QY 185 GILGLGFFILSVRGVPPMDVLVEQGLLDKVPFSFYINRDPEDPDGGELVLGGSDFAHYI 244
 Db 183 GILGLGYPVSLAVGVTVFVDNMAQNLVDLPMFESVYMSSNPEGAGSELIFGGYDHSFHS 242
 QY 245 PPLTFVPTVPAWQHMERVKVPGGLTLCAGCAAILDTGTSITGTEETRALHAAIG 304
 Db 243 GSLNWPVPTKQAYWQIALDNIOVGTVMFCSEGCQAIQVDTGTSITGTSKIKOLQNAIG 302
 QY 305 GIPLLAGEYIILCEIPKLPVAVSFLGGVWFLNTHDYVIOFTRNGVRLCUGSGFOALDV 364
 Db 303 AAR-VGGEYAVECANLNMVDVTFITNGVPTLSPAYTLLDFVDGQMCSSGFGQLDIH 361
 QY 365 PPAGPFWILGDVFLGTVAVVDFDRGDMKKSARVGLARA 401
 Db 362 PPAGPLWILGDVFIKRYYSVFDG-----NNRVGLAPA 394

RESULT 9
 S66465
 cathepsin E (EC 3.4.23.34) precursor (clone pTN05) - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S66465; S74309
 R/Okamoto, K.; Yu, H.; Misumi, Y.; Ikehara, Y.; Yamamoto, K.
 Arch. Biochem. Biophys. 322, 103-111, 1995
 A/Title: Isolation and sequencing of two cDNA clones encoding rat spleen cathepsin E
 A/Reference number: S66465; MUID:96004785; PMID:7574663
 A/Accession: S66465
 A/Molecule type: mRNA
 A/Residues: 1-398 <OKA>
 A/Cross-references: EMBL:D45187; NID:g1113085; PIDN:BAA08128.1; PID:g1113086
 A/Accession: S74309
 A/Molecule type: protein
 A/Residues: 20-47;59-91 <OKW>
 C/Superfamily: pepsin
 C/Keywords: aspartic proteinase; hydrolase
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-58/Domain: propeptide #status experimental <PRO>
 F/59-398/Product: cathepsin E #status experimental <MAT>

Query Match 38.7%; Score 867; DB 2; Length 398;
 Best Local Similarity 45.3%; Pred. No. 1.4e-64;
 Matches 180; Conservative 68; Mismatches 137; Indels 12; Gaps 5;

QY 10 LLLLLLPLNVEPSGATLIRIPHRVQGRRTL----NLLRGWR-EPAELPKLGAPSPGDK 64
 Db 7 LLLLLLLDLAAQGVHLRVPLRRHQSLRKLKLAQGLSDFWKSHNLDIMEFSESCNVDX 66
 QY 65 PIFVPLSNYRDVQYFGEIGLGTTPQNTFVADTGTSSNLNWPVSRCHFFSVPCWLHHRFDP 124
 Db 67 GINEPLINYLDMYFQVTVSIGSPQNTFVIFDTGSSNLNWPVSVYC--TSPACKAHPVFP 124
 QY 125 KASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKAGSVIFGEALWEPVSLVFAFHD 184

R:Panther, J.J.; Foote, S.; Chamberland, B.; Strosberg, A.D.; Corvol, P.; Rougeon, F.
 Nature 298, 90-92, 1982
 A:Title: Complete amino acid sequence and maturation of the mouse submaxillary gland renin
 A:Reference number: A93285; MUID:82220074; PMID:6283373
 A:Accession: A93285
 A:Molecule type: mRNA
 A:Residues: 1-38, 'M', 100-194, 'LSRS', 199-394, 'V', 396-401 <PAL>
 A:Cross-references: GB:J00621; GB:V00845; NID:g200701; PIDN:AAA40050.1; PID:g200702
 A:Note: the authors translated codon ATG for residue 99 as Ile
 A:Accession: B93285
 A:Molecule type: protein
 A:Residues: 64-84; 354-374 <PA2>
 R:Poe, M.; Llesch, J.M.
 J. Biol. Chem. 258, 9856-9860, 1983
 A:Title: Mouse submaxillary gland renin contains a noncovalently attached fatty acid.
 A:Reference number: A92439; MUID:83290909; PMID:6350284
 A:Contents: annotation: fatty acid binding
 R:Panther, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984
 A:Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative region
 A:Reference number: A22058; MUID:84298161; PMID:6089205
 A:Accession: B22058
 A:Molecule type: DNA
 A:Residues: 1-29 <PAN>
 C:Comment: The enzyme contains a noncovalently attached fatty acid.
 C:Comment: Submandibular renin has catalytic and antigenic activities similar to renal renin
 C:Comment: This renin is synthesized in the submandibular gland of males only.
 C:Genetics:
 A:Gene: REN2
 C:Superfamily: pepsin
 C:Keywords: aspartic proteinase; hydrolase; salivary gland; submandibular gland
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-63/Domain: activation peptide #status predicted <ACP>
 F:64-351/Product: renin, submandibular, heavy chain #status experimental <RSH>
 F:354-401/Product: renin, submandibular, light chain #status experimental <RSL>
 F:101,286/Active site: Asp #status experimental
 F:114-121,277-281,320-357/Disulfide bonds: #status predicted

Query Match 36.1%; Score 808.5; DB 1; Length 401;
 Best Local Similarity 41.7%; Pred. No. 1.1e-59;
 Matches 172; Conservative 62; Mismatches 147; Indels 31; Gaps 7;

Qy 5 PLQQLLLLLLNVPSGATLIRIPHRVQPGRTLLNLRGWRPAPLKLGPAP----- 59
 Db 7 PLWALLLWSPCTSLPTGTTFTRIPKKM-PSVREILEERG-----VDMTSLAEWDVFT 61

Qy 60 -----SPGDKPIFVPLSNYRDVQVFGELGTTPQNFVAFDTGSSNLWVPSRCH 110
 Db 62 KRSLTDLISP-----VLTLYNSQYIGELGTTPQNFVAFDTGSSNLWVPSRCH 115

Qy 111 FFSVPCWLHRRFDPKASSFQANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEA 170
 Db 116 RLXLACGIHSLVSSSSSYMEGDDFTHYGSRVKGFLSQDSVTVGGIT-VTQTFGEV 174

Qy 171 LWESLVAFAHFDGILGEPILLSVEGRPMQVLEQGLDKPVSFYLNRPDEPDG 230
 Db 175 TELPLIPMLAQFDGVLGMGFPQAQVGVTFVDFHLSQGVLEKEVFSVYNNRPHLL-G 233

Qy 231 GELVLGGSDPAHYTPPLTFVTPVYQIHMVRKVGGLTLCAGKAAILDGTSLTIT 290
 Db 234 GEVLGGSDPEHYQDGFHYVSLKSDTSWQITMKGVSGSSITLCEEGEVVDVGGSSPIS 293

Qy 291 GPTTEIRALHAAIGGIPILLAGIYILCSEIKPLPAVSFLLGQVFNLFNFAHDYVIQTTRNG 350
 Db 294 APTSSLKIMQALGAKERHLYVVSQVPLPLDISFNLGRAVTLSTDYVLYQPNRR 353

Qy 351 VRLCSLGFQALDVPVPPAGFFVLGTVVAFVDFRGMKSSARVGLAR 402
 Db 354 DKLCTVALHAMDIPPTGFFVVLGATFIRKFTYTFDR-----HNNRIGFALAR 401

RESULT 13
 A43356

cathepsin E (EC 3.4.23.34) precursor - guinea pig
 N:Alternate names: erythrocyte membrane aspartic proteinase; slow-moving proteinase
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 R:Kageyama, T.; Ichinose, M.; Takada, S.; Miki, K.; Kurokawa, K.; Koizumi, O.; Tanji
 J. Biol. Chem. 267, 16450-16459, 1992
 A:Title: Gastric procathepsin E and progastricsin from guinea pig. Purification, mol.
 A:Reference number: A43356; MUID:92355614; PMID:1644829
 A:Accession: A43356
 A:Molecule type: mRNA
 A:Residues: 1-391 <KAG>
 A:Cross-references: GB:M88653; NID:g191294; PIDN:AAA37052.1; PID:g191295
 A:Note: sequence extracted from NCBI backbone (NCBIN:110763, NCBI:110769)
 C:Superfamily: pepsin
 C:Keywords: aspartic proteinase; hydrolase; membrane protein

Query Match 36.0%; Score 806.5; DB 2; Length 391;
 Best Local Similarity 42.8%; Pred. No. 1.6e-59;
 Matches 170; Conservative 72; Mismatches 138; Indels 17; Gaps 7;

Qy 10 LLLLLLPLNVPSGATLIRIPHRVQPGRTLLNLRGWRPAPLKLGPAPSGDK 64
 Db 5 LLLLLLLELQAPCALHRVPLSRSLRKLKRAQGLTELKSNLMDQCSTIQSANE 64

Qy 65 PIFVPLSNYRDVQVFGELGTTPQNFVAFDTGSSNLWVPSRCHPVSFVPCWLHRRPDP 124
 Db 65 ---PLNLYDMVEFGTISGSPFNFTVFDTGSSNLWVSVYC--TSPACQTHPVHP 118

Qy 125 KASSFQANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWPSLVAFAHFD 184
 Db 119 SLSTYREVGNSFIQYGTSLTGIIGADQVSEGLTVVGGQFGESVQEPKTFVHAEFD 178

Qy 185 GILGEPILLSVEGRPMQVLEQGLDKPVSFYLNRPDEPDGGLVLCGSDPAHYI 244
 Db 179 GILGLGFPSLAAGGVTFVDFNMAQNLVAUFPFVSVMSSNP-GSGSELTFGGYDPSHFS 237

Qy 245 PPLTFVTPVYQIHMVRKVGGLTLCAGKAAILDGTSLTITGTEIRALHAAIG 304
 Db 238 GSLNWPVTKQAYWQIALDGLQVDSVWFCEGQAIQVDTGSLTITGPPGKIKQLEALG 297

Qy 305 GIPILLAGIYILCSEIKPLPAVSFLLGQVFNLFNFAHDYVIQTTRNGVRLCSLGFQALDVP 364
 Db 298 ATYYDEG-YSVQCANLNMMLDVTIINGVPTLNTATYLLDFVDGQVCSGTGEGLEIQ 356

Qy 365 PPAGFFVLGTVVAFVDFRGMKSSARVGLARA 401
 Db 357 PFAGPLMLGDFVIRQYVAFVDFRG-----NNRVGLAPA 389

RESULT 14
 S66516
 oryzasin (EC 3.4.23.-) precursor - rice
 N:Alternate names: aspartic proteinase 1
 C:Species: Oryza sativa (rice)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 R:Asakura, T.; Watanabe, H.; Abe, K.; Arai, S.
 Eur. J. Biochem. 232, 77-83, 1995
 A:Title: Rice aspartic proteinase, oryzasin, expressed during seed ripening and germi
 A:Reference number: S66516; MUID:96048031; PMID:7556174
 A:Accession: S66516
 A:Molecule type: DNA
 A:Residues: 1-509 <ASA>
 A:Cross-references: EMBL:D32165; NID:g511665; PIDN:BAA06876.1; PID:g1030715
 A:Accession: S66517
 A:Molecule type: mRNA
 A:Residues: 1-509 <ASZ>
 A:Cross-references: EMBL:D32144; NID:g1255684; PIDN:BAA06875.1; PID:g1711289
 C:Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent
 C:Genetics:
 A:Introns: 119/3; 140/1; 171/3; 209/2; 265/3; 279/1; 300/3; 338/3; 360/2; 412/3; 452/
 C:Superfamily: oryzasin; saposin repeat homology

C;Keywords: aspartic proteinase; hydrolase
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-68/Domain: propeptide #status predicted <PRO>
 F;68-509/Product: aspartic proteinase 1 #status predicted <MAT>
 F;316-361/Domain: saposin repeat homology #status atypical <SAP1>
 F;370-420/Domain: saposin repeat homology #status atypical <SAP2>
 F;103,290/Active site: Asp #status predicted

Query Match 35.9%; Score 804; DB 2; Length 509;
 Best Local Similarity 36.4%; Pred. No. 3.6e-59;
 Matches 185; Conservative 51; Mismatches 146; Indels 126; Gaps 8;

QY	6	LLQPLLLPLLVNPPSGAT--LIRPLHR--VQGRRTNLLRGWRPAELPKLGAPS- 60	
DB	15	LLQALL-----PASAEGLVRLAKKRIDENSRVAARLSGEGARRLGLAGANSL 65	
QY	61	--PGDKPIVPLNSNRDVOYGEIGLGTTPQNFTVAFTGSSNLWVPSRRCHFFSVPCWL 118	
DB	66	GGGGGEGDVALKNTYMAQYFGEIGVGTTPQKFTVFDTGSSNLWVPSAKC-YFSIACFF 124	
QY	119	HRFDPKASSFCANGTKFAIOYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVF 178	
DB	125	HSRYKSGQSTYQKNGKPAAIQYGTGSIAGFFSEDSVTGDLVVKDQEFIEATKEPGLTF 184	
QY	179	AFAFEDGILGLGFPILSVGVRPPMDVLVEQGLLQKPFVFIYNRDPPEPDGGLVGLGS 238	
DB	185	MYAKFDGILGLGFEISVGDVAVPMYKVEQGLVSEPVFSFWNRHSDSGEGEIVFGQM 244	
QY	239	DPAHYIPPLTFVTVPAQVQIHMERYKVGPGLT-LCAKGCAAILDTGSLTGTTEER 297	
DB	245	DPHYKGNHTYVFSVQKGYQFEMGDVLIGGKTTGFCASGCSAIAADSGTSLLAGPTAIT 304	
QY	298	ALHAAATG----- 305	
DB	305	EINEKIGATGVWSQBEKTVVSQYGOQIILLIAETOPSKICQVGLCTDGHKGVSAIK 364	
QY	306	-----IPLLAGY 313	
DB	365	SVVDDRAGESNGLSQGMNACEMAVVMQNQLAQNKTQDLILNYINQLCDKLPSPMGES 424	
QY	314	IILCSIPKLPVAVSFLGGVWNLTAHDYVIOYTRNGVRLCLSGFOALDVPVPPAGFWIL 373	
DB	425	SVDCGSLASMPETISFTIGAKKFAKPEEYILKVGEGAAAQCISSGTAMDIPPRGFLWIL 484	
QY	374	GDVFLGTVAVFDGDMKSSARVGLARA 401	
DB	485	GDVFMGAYHTVFDYGM-----RVGFAS 508	

RESULT 15
 JC5077
 aspartic proteinase (EC 3.4.23.-) - dog hookworm (Ancylostoma caninum) (fragment)
 N;Alternate names: Acasp; cathepsin D homolog
 C;Species: Ancylostoma caninum
 C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999
 C;Accession: JC5077
 R;Harrop, S.A.; Procliv, P.; Brindley, P.J.
 Biochem. Biophys. Res. Commun. 227, 294-302, 1996
 A;Title: Acasp, a gene encoding a cathepsin D-like aspartic protease from the hookworm
 A;Reference number: JC5077; MUID:97011129; PMID:8858139
 A;Accession: JC5077
 A;Molecule type: mRNA
 A;Residues: 1-442 <HAR>
 A;Cross-references: GB:U34888; NID:G1507724; PIDN:AAB06575.1; PID:G1507725
 C;Comment: This enzyme is allergenic in human and contributes to the segmental inflammation
 C;Genetics:
 A;Gene: Acasp
 C;Superfamily: pepsin
 C;Keywords: aspartic proteinase; hydrolase
 F;106,296/Active site: Asp #status predicted

Query Match 35.9%; Score 803.5; DB 2; Length 442;
 Best Local Similarity 47.5%; Pred. No. 3.3e-59;

Matches	160;	Conservative	44;	Mismatches	126;	Indels	7;	Gaps	2;
QY	70	LSNYRDVOYGEIGLGTTPQNFTVAFTGSSNLWVPSRRCHFFSVPCWLHRRFDPKASSS 129							
DB	80	LRTWMDAQYFTGIQIGTPAQNFVIFDTGSSNLWVPSRRCHFFHDIACMLRHYDSGASST 139							
QY	130	FOANGTKFAIOYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFVFAHFDGILGL 189							
DB	140	YKEDGRKMAIOYGTGSMKGFISKDNVCIAGICAEQPAEATSEPLTFFIAAKFDGILGI 199							
QY	190	GFPILSVGVRPPMDVLVEQGLLQKPFVFIYNRDPPEPDGGLVGLGSDDPAHVIPPLTF 249							
DB	200	TFPEISVLGVPPVFHTFIEQKKVSPFALMLNRPDSELGGEITLGGMDTRRIVEPLTW 259							
QY	250	VPVTVPAQVQIHMERYKVGPGLTICA---KGC AAILDTGSLTGTTEERIALHAAIGGI 306							
DB	260	TPVTRGYWQFKMDKVQGGSTSIACPNFSCQAIADTGTSLIAGPKAQSASRNSLVLE 319							
QY	307	PLLAGEYIILCSEIPKLPVAVSFLGGVWNLTAHDYVIOYTRNGVRLCLSGFOALDVPVPP 366							
DB	320	PTYEGEYMPCDKVPFPPLSFVIEARTFTLKGEDYVLTVKAGGKSIKLSGFMGMDFPER 379							
QY	367	AGPFWILGDVFLGTVAVFDGDMKSSARVGLARAT 403							
DB	380	IGELMILGDVFIGKYYTVFDVG-----QARLGFAQAKS 412							

Search completed: June 2, 2004, 20:22:21
 Job time : 29.59 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 20:19:10 ; Search time 74.8784 Seconds
(without alignments)
1578.054 Million cell updates/sec

Title: US-09-700-770-8

Perfect score: 2238

Sequence: 1 MSPPPPLQLPLLLPLLNVE.....ARTRGADLGMGTAAQFPG 420

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/PCT_US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2238	100.0	420	12	US-09-968-415-4
2	2238	100.0	420	14	US-10-180-719-4
3	2232	99.7	420	14	US-10-288-222A-30
4	2232	99.7	433	9	US-09-964-899-11
5	2069.5	92.5	393	13	US-10-094-080-3
6	1702.5	76.1	390	9	US-09-969-384-15
7	1560.5	69.7	419	9	US-09-789-919-44
8	1328	59.3	262	9	US-09-915-582-66
9	1328	59.3	262	11	US-09-833-245-1469
10	1328	59.3	262	14	US-10-277-802-66
11	1179	52.7	285	9	US-09-925-302-670
12	1179	52.7	285	12	US-09-925-302-670
13	1050	46.9	212	9	US-09-915-582-87
14	1050	46.9	212	11	US-09-833-245-1471
15	1050	46.9	212	14	US-10-277-802-87

16	1037	46.3	410	11	US-09-833-245-710
17	1015	45.4	412	9	US-09-215-450-25
18	1015	45.4	412	9	US-09-953-956-12
19	1015	45.4	412	12	US-10-275-107-39
20	1015	45.4	412	13	US-10-114-464-12
21	1015	45.4	412	16	US-10-601-091-25
22	1015	45.4	412	16	US-10-408-765A-406
23	1002	44.8	440	12	US-10-112-944-433
24	905.5	40.5	444	15	US-10-369-493-6962
25	887	39.6	446	14	US-10-220-083-2
26	869	38.8	396	9	US-09-215-450-22
27	869	38.8	396	9	US-09-953-956-13
28	869	38.8	396	12	US-10-621-263-9
29	869	38.8	396	13	US-10-114-464-13
30	869	38.8	396	15	US-10-295-027-179
31	869	38.8	396	16	US-10-188-832-54
32	869	38.8	396	16	US-10-601-091-22
33	868	38.8	368	11	US-09-833-245-707
34	868	38.8	404	14	US-10-106-698-6317
35	828.5	37.0	514	14	US-10-339-351-1
36	825.5	36.9	514	14	US-10-339-351-3
37	815	36.4	507	12	US-10-424-599-245585
38	798.5	35.7	523	12	US-10-425-114-57691
39	793	35.4	376	15	US-10-051-874-164
40	790	35.3	374	15	US-10-074-978A-134
41	788	35.2	513	12	US-10-425-114-46548
42	788	35.2	513	12	US-10-425-114-66071
43	787	35.2	480	12	US-10-425-114-65101
44	787	35.2	513	12	US-10-425-114-56631
45	786	35.1	513	12	US-10-425-114-57054

ALIGNMENTS

RESULT 1

US-09-968-415-4
; Sequence 4, Application US/09968415
; Publication No. US20020086334A1
; GENEAL INFORMATION:
; APPLICANT: Handman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,415
; FILING DATE: 26-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/659,151
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555

Sequence 710, Appl
Sequence 25, Appl
Sequence 12, Appl
Sequence 39, Appl
Sequence 12, Appl
Sequence 25, Appl
Sequence 406, Appl
Sequence 433, Appl
Sequence 6962, Appl
Sequence 2, Appl
Sequence 22, Appl
Sequence 13, Appl
Sequence 9, Appl
Sequence 13, Appl
Sequence 179, Appl
Sequence 54, Appl
Sequence 22, Appl
Sequence 707, Appl
Sequence 6317, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 245585,
Sequence 57691, A
Sequence 164, Appl
Sequence 134, Appl
Sequence 46548, A
Sequence 66071, A
Sequence 65101, A
Sequence 56631, A
Sequence 57054, A

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;
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGAST01
; CLONE: 877617
; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
US-09-968-415-4

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Best Local Similarity 100.0%; Pred. No. 1.9e-209;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSPPPLQLQLLLPLLNVEPSGATLIRIPLHRVQPGRTNLLRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYRDVQYFGEIGLGTTPQNFTVAEDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNRYRDVQYFGEIGLGTTPQNFTVAEDTGSSNLWVPSRRCHFFSVPCWLHH 120

QY 121 RFDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGKASVIFGEALWEPSSLVFAF 180
Db 121 RFDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGKASVIFGEALWEPSSLVFAF 180

QY 181 AHFDGILGLGFFILSVGVRPMDVLVEQGLDKPVFSFYLNRDPEPDGGLVLGGSDP 240
Db 181 AHFDGILGLGFFILSVGVRPMDVLVEQGLDKPVFSFYLNRDPEPDGGLVLGGSDP 240

QY 241 AHYIPLTFVPTVPAYQIHMERYKVGGLTLCAKGCALDGTSLITGTEIRALH 300
Db 241 AHYIPLTFVPTVPAYQIHMERYKVGGLTLCAKGCALDGTSLITGTEIRALH 300

QY 301 AAGGIPPLAGEYIILCSSEIPKLPVAVSFLGGVWENLTAHDYVIQTRNGVRLCLSGFOA 360
Db 301 AAGGIPPLAGEYIILCSSEIPKLPVAVSFLGGVWENLTAHDYVIQTRNGVRLCLSGFOA 360

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RESULT 2

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US-10-180-719-4
; Sequence 4, Application US/10180719
; Publication No. US20030166246A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guégler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi.
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/10/180,719
; FILING DATE: 25-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271
; FILING DATE: 16-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGAST01
; CLONE: 877617
; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
US-10-180-719-4
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Query Match 100.0%; Score 2238; DB 14; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.9e-209;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSPPPLQLQLLLPLLNVEPSGATLIRIPLHRVQPGRTNLLRGWREPAELPKLGAPS 60

QY 61 PGDKPIFVPLSNRYRDVQYFGEIGLGTTPQNFTVAEDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNRYRDVQYFGEIGLGTTPQNFTVAEDTGSSNLWVPSRRCHFFSVPCWLHH 120

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Db 121 RFDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGKASVIFGEALWEPSSLVFAF 180

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Db 181 AHFDGILGLGFFILSVGVRPMDVLVEQGLDKPVFSFYLNRDPEPDGGLVLGGSDP 240

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RESULT 3

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US-10-288-222A-30
; Sequence 30, Application US/10288222A
; Publication No. US20030119742A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Galvin, Katherine
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: Methods and Compositions to treat
; TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 241
; FILE REFERENCE: MPI2001-286PIR(M)
; CURRENT APPLICATION NUMBER: US/10/288,222A
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 30
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-288-222A-30

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Best Local Similarity 99.8%; Pred. No. 7.3e-209;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
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DB 301 AATGGIPLLAGETIILCSEIPKLPVAVSFLGGVWFLTAHDYVIQTRNGVRLCLSGFOA 360
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RESULT 4
US-09-964-899-11
; Sequence 11, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-11

Query Match      99.7%; Score 2232; DB 9; Length 433;
Best Local Similarity 99.8%; Pred. No. 7.6e-209;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 14 MSPPPLLOPLLLLLPLLNVEPSGATLIRIPLHRVQPGRTNLRGWRPAPLKLKGLAPS 73
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; SEQ ID NO 121
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-094-080-3

Query Match      99.7%; Score 2232; DB 14; Length 420;
Best Local Similarity 99.8%; Pred. No. 7.3e-209;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
DB 134 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 193
QY 181 AHFDGILGLGFPILLSVEGRPPMDVLVBOGLDKPVSFYLNDRDPPEPDGGLVILGSDP 240
DB 194 AHFDGILGLGFPILLSVEGRPPMDVLVBOGLDKPVSFYLNDRDPPEPDGGLVILGSDP 253
QY 241 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALH 300
DB 254 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALH 313
QY 301 AATGGIPLLAGETIILCSEIPKLPVAVSFLGGVWFLTAHDYVIQTRNGVRLCLSGFOA 360
DB 314 AATGGIPLLAGETIILCSEIPKLPVAVSFLGGVWFLTAHDYVIQTRNGVRLCLSGFOA 373
QY 361 LDVPPPPAGPWILGDVFLGTVAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFPG 420
DB 374 LDVPPPPAGPWILGDVFLGTVAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFPG 433

RESULT 5
US-10-094-080-3
; Sequence 3, Application US/10094080
; Publication No. US20020187140A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/094,080
; FILING DATE: 07-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/387,413
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0125 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; LIBRARY: LUNGN020
; CLONE: 312099
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
```


US-10-094-080-3

Query Match 92.5%; Score 2069.5; DB 13; Length 395;
 Best Local Similarity 93.8%; Pred. No. 4.8e-193;
 Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;
 QY 1 MSPPPLOPLLLPLLVNPSGATLIRIPLHRVQGRRTLLNLRGWREPAELPKLGAPS 60
 DB 1 MSPPPLOPLLLPLLVNPSGATLIRIPLHRVQGRRTLLNLRGWREPAELPKLGAPS 60
 QY 61 PGDKPIFVPLSNRYRDVQFGEIGLTPPQNFVAEDTSSNLWPSRRCHFFSVPCWLHH 120
 DB 61 PGDKPIFVPLSNRYRDVQFGEIGLTPPQNFVAEDTSSNLWPSRRCHFFSVPCWLHH 120
 QY 121 RFPDKASSFOANGKFAIQGTGRVDGILSDKLTIGIKGASVIFGEALWERSLVFAF 180
 DB 121 RFPDKASSFOANGKFAIQGTGRVDGILSDKLTIGIKGASVIFGEALWERSLVFAF 180
 QY 181 AHFDGILGFPILSVGVRRPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGSDP 240
 DB 181 AHFDGILGFPILSVGVRRPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGSDP 240
 QY 241 AHYIPLTFVPTVAYQIHMERVKVGPGTLCAKGCALIDTGTSLITGTEIRALH 300
 DB 241 AHYIPLTFVPTVAYQIHMERVKVGPGTLCAKGCALIDTGTSLITGTEIRALH 300
 QY 301 AAIGGIPLAGBYIILCSEIPKLPVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 360
 DB 301 AAIGGIPLAGBYIILCSEIPKLPVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 360
 QY 361 LDVPPPAGEFWILGDVFTGYVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 420
 DB 361 LDVPPPAGEFWILGDVFTGYVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 420
 QY 395 -----DVFLGTYVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 395

RESULT 6

US-09-969-384-15
 ; Sequence 15, Application US/09969384
 ; Publication No. US20020192749A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Moore, et al.
 ; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
 ; FILE REFERENCE: PT055PI
 ; CURRENT APPLICATION NUMBER: US/09/969,384
 ; PRIOR FILING DATE: 2001-10-03
 ; PRIOR APPLICATION NUMBER: PCT/US01/10542
 ; PRIOR FILING DATE: 2001-04-02
 ; PRIOR APPLICATION NUMBER: 60/236,384
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/194,118
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 390
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-969-384-15
 Query Match 76.1%; Score 1702.5; DB 9; Length 390;
 Best Local Similarity 83.3%; Pred. No. 3.1e-157;
 Matches 334; Conservative 7; Mismatches 15; Indels 45; Gaps 4;
 QY 21 PSGATLIRIPLHRVQGRRTLLNLRGWREPAELPKLGAPSGDKPIFVPLSNRYRDVQYFG 80
 DB 34 PSGATLIRIPLHRVQGRRTLLNLRGWREPAELPKLGAPSGDKPIFVPLSNRYK 88
 QY 81 EIGLGTTPQNFVAEDTSSNLWPSRRCHFFSVPCWLHHRFDPKASSFOANGKFAIQ 140
 DB 89 -----WLHHRFDPKASTP-SSQWDQFAIQ 111
 QY 141 YGTGRVDGILSDKLTIGIKGASVIFGE-ALWERSLVFAFAHFDGILGFPILSVGV 199

DB 112 YGTGRVHGILSDKLTIGIKGASVIFGEALSGTQFGL--RFPDPPDGLGGLFPILSVGV 169
 QY 200 RPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGSDPAHYIPLTFVPTVTPAYWQ 259
 DB 170 RPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGSDPAHYIPLTFVPTVTPAYWQ 229
 QY 260 IHMERVKVGPGLTICAKGCAAILDTGTSLITGPTTEIRALHAAIGGIPLLAGYIILCSE 319
 DB 230 IHMERVKVGPGLTICAKGCAAILDTGTSLITGPTTEIRALHAAIGGIPLLAGYIILCSE 289
 QY 320 IPKLPVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 420
 DB 290 IPKLPVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 390
 QY 380 TYVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 420
 DB 350 TYVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 390
 RESULT 7
 US-09-783-919-44
 ; Sequence 44, Application US/09789919
 ; Patent No. US2002006485A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lemischka, Ihor
 ; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
 ; FILE REFERENCE: 2275-1-005
 ; CURRENT APPLICATION NUMBER: US/09/789,919
 ; CURRENT FILING DATE: 2001-02-21
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 44
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-783-919-44
 Query Match 69.7%; Score 1560.5; DB 9; Length 419;
 Best Local Similarity 70.3%; Pred. No. 2.5e-143;
 Matches 296; Conservative 37; Mismatches 79; Indels 9; Gaps 3;
 QY 7 LQPLLLPLLL---NVPSGATLIRIPLHRVQGRRTLLNLRGWREPAELPKLGAPSGD 63
 DB 1 MSPLLLLCLLLNLEPEEAKLIRVPLQRIHLGHRILNPLNGWEQLAELSR--TSTSGG 58
 QY 64 KPIFVPLSNRYRDVQFGEIGLTPPQNFVAEDTSSNLWPSRRCHFFSVPCWLHHRFD 123
 DB 59 NPSFVPLSKFMNTQYFGTIGLTPPQNFVAEDTSSNLWPSRRCHFFSVPCWLHHRFD 118
 QY 124 PKASSFOANGKFAIQGTGRVDGILSDKLTIGIKGASVIFGEALWERSLVFAFAHF 183
 DB 119 PKASSFRPNTGKFAIQGTGRVLSGLISQDNLITGIIHDAFVTFGEALWERSLVFAFAHF 178
 QY 184 DGILGFPILSVGVRRPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGSDPAHY 243
 DB 179 DGILGFPILSVGVRRPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGSDPAHY 238
 QY 244 IPIPLTFVPTVAYQIHMERVKVGPGTLCAKGCALIDTGTSLITGTEIRALHAAI 303
 DB 239 VPPLTFIPIPTVAYQVHVESVKGVTGSLCAQGSAILDTGTSLITGTEIRALHAAI 298
 QY 304 GGIPPLAGBYIILCSEIPKLPVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 363
 DB 299 GGPYPLNGYFQCSKTPPLPVPSFHLGVMFNLTQDQVYIKILQSDVGLCLLGFQALDI 358
 QY 364 PPAAGFWILGDVFTGYVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP----P 419
 DB 359 PKPAGFWILGDVFTGYVAVFDRGDMKSSARVGLARTRGADLGWGETAQAFP 418
 QY 420 G 420

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Db 419 G 419
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1469
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (231)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-1469

Query Match 59.3%; Score 1328; DB 11; Length 262;
Best Local Similarity 97.6%; Pred. No. 6.2e-121;
Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPHRVQPGRRITNLLRGWREPAELPKLGAPS 60
Db 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPHRVQPGRRITNLLRGWREPAELPKLGAPS 60
Qy 61 PGDKPIFVPLSNYRDVQYFGIIGLTPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNYRDVQYFGIIGLTPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Qy 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPSLVFAF 180
Db 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPSLVFAF 180
Qy 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLDKPVFSFYLNRPDPEPDGGELVLGGSDP 240
Db 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLDKPVFSFYLNRPDPEPDGGELVLGGSDP 240
Qy 241 AHYIPPLTFVPTVP 255
Db 241 AHYIPPSFFVVRSP 255

RESULT 10
US-10-277-802-66
; Sequence 66, Application US/10277802
; Publication No. US2003019070A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723p1
; CURRENT APPLICATION NUMBER: US/10/277,802
; CURRENT FILING DATE: 2002-10-23
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (231)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-277-802-66

Query Match 59.3%; Score 1328; DB 14; Length 262;
Best Local Similarity 97.6%; Pred. No. 6.2e-121;
Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPHRVQPGRRITNLLRGWREPAELPKLGAPS 60
Db 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPHRVQPGRRITNLLRGWREPAELPKLGAPS 60
Qy 61 PGDKPIFVPLSNYRDVQYFGIIGLTPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNYRDVQYFGIIGLTPQNTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Qy 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPSLVFAF 180
Db 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWEPSLVFAF 180
Qy 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLDKPVFSFYLNRPDPEPDGGELVLGGSDP 240
Db 181 AHFDGILGLGFPILSVGVRRPMDVLVEQGLDKPVFSFYLNRPDPEPDGGELVLGGSDP 240
Qy 241 AHYIPPLTFVPTVP 255
Db 241 AHYIPPSFFVVRSP 255

RESULT 9
US-09-833-245-1469
; Sequence 1469, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
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QY 1 MSPBPLOPLLLPLLVESGATLIRIPLRHVQPGRTTLNLRGWREPAELPKLGAPS 60
Db 1 MSPBPLOPLLLPLLVESGATLIRIPLRHVQPGRTTLNLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
QY 121 RPDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGIKASVIFGEALWEPVSLVFAF 180
Db 121 RPDPKASSFQANGTKFAIQYGTGRVDGLSDKLTIGGIKASVIFGEALWEPVSLVFAF 180
QY 181 AHFDGILGLGFPILSVGEVVRPMDVLEQGLLDKPVFSFYLNRPDEEPPDGXELVLGSDP 240
Db 181 AHFDGILGLGFPILSVGEVVRPMDVLEQGLLDKPVFSFYLNRPDEEPPDGXELVLGSDP 240
QY 241 AHYIPPLTFVPTVP 255
Db 241 AHYIPSPFVVRSP 255

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RESULT 11
US-09-925-302-670
; Query Match 52.7%; Score 1179; DB 9; Length 285;
; Best Local Similarity 80.7%; Pred. No. 2.4e-106;
; Matches 230; Conservative 4; Mismatches 9; Indels 42; Gaps 2;
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 670
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-670

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QY 21 PSGATLIRIPLRHVQPGRTTLNLRGWREPAELPKLGAPSPGDKPIFVPLSNRYDVQYFG 80
Db 43 PSGATLIRIPLRHVQPGRTTLNLRGWREPAELPKLGAPSPGDKPIFVPLSNYKG----- 97
QY 81 EIGLGTTPQNFVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSFQANGTKFAIQ 140
Db 98 -----WLHHRFDPKASTP-SSQWDQFAIQ 120
QY 141 YGTGRVDGILSEDKLTIGGIKASVIFGEALWEPVSLVFAFHFDGILGFPILSVGEVR 200
Db 121 YGTGRVHGILSEDKLTIGGIKASVIFGEALWEPVSLVFAFHFDGILGFPILSVGEVR 180
QY 201 PMDVLVEQGLLDKPVFSFYLNRPDEEPPDGXELVLGSDPAHYIPPLTFVPTVPYAWQI 260
Db 181 PMDVLVEQGLLDKPVFSFYLNRPDEEPPDGXELVLGSDPAHYIPPLTFVPTVPYAWQI 240
QY 261 HMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALHAAIGG 305
Db 241 HMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALHAAIGG 285

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RESULT 12
US-09-925-302-670
; Sequence 670, Application US/09925302
; Publication No. US20030064072A9

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 670
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-670

```

```

Query Match 52.7%; Score 1179; DB 12; Length 285;
Best Local Similarity 80.7%; Pred. No. 2.4e-106;
Matches 230; Conservative 4; Mismatches 9; Indels 42; Gaps 2;
QY 21 PSGATLIRIPLRHVQPGRTTLNLRGWREPAELPKLGAPSPGDKPIFVPLSNRYDVQYFG 80
Db 43 PSGATLIRIPLRHVQPGRTTLNLRGWREPAELPKLGAPSPGDKPIFVPLSNYKG----- 97
QY 81 EIGLGTTPQNFVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSFQANGTKFAIQ 140
Db 98 -----WLHHRFDPKASTP-SSQWDQFAIQ 120
QY 141 YGTGRVDGILSEDKLTIGGIKASVIFGEALWEPVSLVFAFHFDGILGFPILSVGEVR 200
Db 121 YGTGRVHGILSEDKLTIGGIKASVIFGEALWEPVSLVFAFHFDGILGFPILSVGEVR 180
QY 201 PMDVLVEQGLLDKPVFSFYLNRPDEEPPDGXELVLGSDPAHYIPPLTFVPTVPYAWQI 260
Db 181 PMDVLVEQGLLDKPVFSFYLNRPDEEPPDGXELVLGSDPAHYIPPLTFVPTVPYAWQI 240
QY 261 HMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALHAAIGG 305
Db 241 HMERVKVGPGLTLCAGCAAILDTGTSITGPTTEIRALHAAIGG 285

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RESULT 13
US-09-915-582-87
; Sequence 87, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-915-582-87

```

Query Match 46.9%; Score 1050; DB 9; Length 212;
 Best Local Similarity 100.0%; Pred. No. 6.2e-94;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 283
 DB 16 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 75

QY 284 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 343
 DB 76 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 135

QY 344 IQTTRNGVRLCLSGFQALDVPVPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARART 403
 DB 136 IQTTRNGVRLCLSGFQALDVPVPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARART 195

QY 404 RGADLWGGETAQAFPG 420
 DB 196 RGADLWGGETAQAFPG 212

RESULT 14

US-09-833-245-1471
 ; Sequence 1471, Application US/09833245
 ; Publication No. US20040010134A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: Albumin Fusion Proteins
 ; FILE REFERENCE: PF546FCT
 ; CURRENT APPLICATION NUMBER: US/09/833,245
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/229,358
 ; PRIOR FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: 60/256,931
 ; PRIOR FILING DATE: 2000-12-21
 ; PRIOR APPLICATION NUMBER: 60/199,384
 ; PRIOR FILING DATE: 2000-04-25
 ; NUMBER OF SEQ ID NOS: 2267
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1471
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (9)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Query Match 46.9%; Score 1050; DB 11; Length 212;
 Best Local Similarity 100.0%; Pred. No. 6.2e-94;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 283
 DB 16 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 75

QY 284 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 343
 DB 76 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 135

QY 344 IQTTRNGVRLCLSGFQALDVPVPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARART 403
 DB 136 IQTTRNGVRLCLSGFQALDVPVPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARART 195

QY 404 RGADLWGGETAQAFPG 420
 DB 196 RGADLWGGETAQAFPG 212

RESULT 15

US-10-277-802-87
 ; Sequence 87, Application US/10277802

Publication No. US20030190707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 17 Human Secreted Proteins
 ; FILE REFERENCE: PS723P1
 ; CURRENT APPLICATION NUMBER: US/10/277,802
 ; CURRENT FILING DATE: 2002-10-23
 ; PRIOR APPLICATION NUMBER: 09/915,582
 ; PRIOR FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/01431
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 60/179,065
 ; PRIOR FILING DATE: 2000-01-31
 ; PRIOR APPLICATION NUMBER: 60/180,628
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: 60/231,968
 ; PRIOR FILING DATE: 2000-09-12
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 87
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (9)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-277-802-87

Query Match 46.9%; Score 1050; DB 14; Length 212;
 Best Local Similarity 100.0%; Pred. No. 6.2e-94;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 283
 DB 16 DPEPDGGLVGGSDPAHYIPPLTFVPTVPAYWQHMERVKVGPGLTLCAGCAAILD 75

QY 284 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 343
 DB 76 TGTSLITGPTTEIRALHAAIGGIPLLAGEYIILCSEIPKLPAYSVFLGGVWFNLTADYV 135

QY 344 IQTTRNGVRLCLSGFQALDVPVPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARART 403
 DB 136 IQTTRNGVRLCLSGFQALDVPVPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARART 195

QY 404 RGADLWGGETAQAFPG 420
 DB 196 RGADLWGGETAQAFPG 212

Search completed: June 2, 2004, 20:25:19
 Job time : 75.8784 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 20:16:40 ; Search time 29.2707 Seconds
(without alignments)
740.773 Million cell updates/sec

Title: US-09-700-770-8
Perfect score: 2238
Sequence: 1 MSPPPLQLPLLLLLLNVE.....ARTRGADLGNGETAQAQFFG 420

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2238	100.0	420	3	US-09-008-271A-4
2	2238	100.0	420	4	US-09-705-448-1
3	2232	99.7	420	3	US-08-974-691-8
4	2069.5	92.5	395	1	US-08-723-338-3
5	2069.5	92.5	395	2	US-09-080-538-3
6	2069.5	92.5	395	4	US-09-387-413-3
7	1897	84.8	445	3	US-08-974-691-6
8	1897	84.8	451	3	US-08-974-691-2
9	1877	83.9	433	4	US-09-705-448-3
10	1564.5	69.9	419	3	US-08-974-691-3
11	1560.5	69.7	419	4	US-09-705-448-10
12	1015	45.4	412	1	US-08-208-007A-12
13	1015	45.4	412	3	US-08-974-691-4
14	1015	45.4	412	4	US-08-915-035A-12
15	1015	45.4	412	4	US-08-798-096-12
16	1015	45.4	412	4	US-08-798-095A-12
17	1015	45.4	412	4	US-09-953-956-12
18	1015	45.4	412	4	US-08-553-125A-12
19	1015	45.4	412	4	US-09-215-450-25
20	1015	45.4	412	4	US-10-114-464-12
21	869	38.8	386	1	US-08-208-007A-13
22	869	38.8	396	3	US-09-032-523-9
23	869	38.8	396	4	US-08-915-095A-13
24	869	38.8	396	4	US-08-798-096-13
25	869	38.8	396	4	US-08-798-095A-13
26	869	38.8	396	4	US-09-953-956-13
27	869	38.8	396	4	US-08-553-125A-13

28	869	38.8	396	4	US-09-802-633-9	Sequence 9, Appli
29	869	38.8	396	4	US-09-215-450-22	Sequence 22, Appli
30	869	38.8	396	4	US-10-114-464-13	Sequence 13, Appli
31	779	34.8	406	4	US-09-215-450-26	Sequence 26, Appli
32	759.5	33.9	388	4	US-09-215-450-23	Sequence 23, Appli
33	729	32.6	326	4	US-09-604-608-31	Sequence 31, Appli
34	708.5	31.7	349	3	US-09-032-523-3	Sequence 3, Appli
35	708.5	31.7	349	4	US-09-802-633-3	Sequence 3, Appli
36	705.5	31.5	398	1	US-08-328-314-2	Sequence 2, Appli
37	705.5	31.5	398	1	US-08-731-045-2	Sequence 2, Appli
38	693.5	31.0	409	1	US-09-640-305-6	Sequence 6, Appli
39	693.5	31.0	409	1	US-08-360-673-6	Sequence 6, Appli
40	691.5	30.9	397	3	US-09-079-415-2	Sequence 24, Appli
41	668.5	29.9	388	4	US-09-215-450-24	Sequence 2, Appli
42	666	29.8	410	1	US-08-088-633-2	Sequence 2, Appli
43	666	29.8	410	1	US-08-245-756-2	Sequence 2, Appli
44	666	29.8	410	1	US-08-441-750-2	Sequence 2, Appli
45	666	29.8	410	2	US-08-441-751-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-008-271A-4
; Sequence 4, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Shesha
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNCAST01
; CLONE: 877617
; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
US-09-008-271A-4

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Best Local Similarity 100.0%; Pred. No. 2e-222;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120

QY 121 RFDPKASSFOANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPFLVAF 180
DB 121 RFDPKASSFOANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPFLVAF 180

QY 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLDKPVSFYLNRPDPPEPDGSELVLGSDP 240
DB 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLDKPVSFYLNRPDPPEPDGSELVLGSDP 240

QY 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGTLCAKCAAILDTGTSLTITGPTTEIRALH 300
DB 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGTLCAKCAAILDTGTSLTITGPTTEIRALH 300

QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVFDGMDKSSARVGLARARTGADLGMGTAAQPPG 420
DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVFDGMDKSSARVGLARARTGADLGMGTAAQPPG 420

RESULT 2

US-09-705-448-1
; Sequence 1, Application US/09705448
; Patent No. 6432690
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Bruno, Sandra A.
; APPLICANT: Eisenboos, Laura A.
; APPLICANT: Fogliano, Michael
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES
; FILE REFERENCE: PF-0458-1 CIP
; CURRENT APPLICATION NUMBER: US/09/705,448
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/116,641
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/008,271
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: 372637, LUNGNOT02
US-09-705-448-1

Query Match 100.0%; Score 2238; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 2e-222;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRTNLLRGWREPAELPKLGAPS 60

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DB 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120

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DB 121 RFDPKASSFOANGTKFAIQYGTGRVDGILSDKLTIGIKGASVIFGEALWEPFLVAF 180

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DB 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLDKPVSFYLNRPDPPEPDGSELVLGSDP 240

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DB 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGTLCAKCAAILDTGTSLTITGPTTEIRALH 300

QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVFDGMDKSSARVGLARARTGADLGMGTAAQPPG 420

DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVFDGMDKSSARVGLARARTGADLGMGTAAQPPG 420

RESULT 3

US-08-974-691-8
; Sequence 8, Application US/08974691
; Patent No. 6225103
; GENERAL INFORMATION:
; APPLICANT: Keolach, Gerald
; APPLICANT: Lin, Xinli
; APPLICANT: Tang, Jordan
; TITLE OF INVENTION: Cloning and Characterization of Napsin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; STREET: St.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,691
; FILING DATE: 20-NOV-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,196
; FILING DATE: 20-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,126
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-974-691-8

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Query Match          99.7%; Score 2232; DB 3; Length 420;
Best Local Similarity 99.8%; Pred. No. 8.5e-222;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MSPPPQLQPLLLPLLNVEPSGATLIRIPLHRVQPGRRITNLLRGWREPAELPKLGAPS 60
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DB 61 PGDKPIFVPLSNRYDVOYGEIGLGTTPQNTFAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
QY 121 RFPDKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
DB 121 RFPDKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
QY 181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNDRDPEPDGGLVLGGSDP 240
DB 181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNDRDPEPDGGLVLGGSDP 240
QY 241 AHYIPPLTFVPVTPAYWQIHMERSVKVPGGLTICAKGCAAILDTGTSITGPTTEIRALH 300
DB 241 AHYIPPLTFVPVTPAYWQIHMERSVKVPGGLTICAKGCAAILDTGTSITGPTTEIRALH 300
QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTADHYVIQTTRNGVRLCLSGFOA 360
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QY 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFPG 420
DB 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFPG 420

RESULT 4
US-08-723-938-3
; Sequence 3, Application US/08723938
; Patent No. 5776759
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,938
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0125 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
LIBRARY: LUNGN0T02
CLONE: 312099
US-08-723-938-3

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Best Local Similarity 93.8%; Pred. No. 4.6e-205;
Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

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DB 61 PGDKPIFVPLSNRYDVOYGEIGLGTTPQNTFAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
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DB 121 RFPDKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWEPSSLVFAF 180
QY 181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNDRDPEPDGGLVLGGSDP 240
DB 181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNDRDPEPDGGLVLGGSDP 240
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DB 241 AHYIPPLTFVPVTPAYWQIHMERSVKVPGGLTICAKGCAAILDTGTSITGPTTEIRALH 300
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DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTADHYVIQTTRNGVRLCLSGFOA 360
QY 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFPG 420
DB 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARTRGADLWGGETAQAOFPG 420

RESULT 5
US-09-080-538-3
; Sequence 3, Application US/09080538
; Patent No. 5965129
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,538
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/723,938
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0125 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT02
; CLONE: 312099
; US-09-080-538-3

Query Match          92.5%; Score 2069.5; DB 2; Length 395;
Best Local Similarity 93.8%; Pred. No. 4.6e-205;
Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

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DB 1 MSPPPQLQPLLLLLPLLNVPESGATLIRPLHRVQPGRRITNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNYRDVQVFEIGLTGTPQNFTVAEDTGSNNLWVPSRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNYRDVQVFEIGLTGTPQNFTVAEDTGSNNLWVPSRCHFFSVPCWLHH 120
QY 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPVSLVAF 180
DB 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPVSLVAF 180
QY 181 AHFDGILGFPILSVEGVRRPMDVLEQGLLDKVPFSPYLNRPDEPDGGLVILGSDP 240
DB 181 AHFDGILGFPILSVEGVRRPMDVLEQGLLDKVPFSPYLNRPDEPDGGLVILGSDP 240
QY 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGITLCAKGCALDITGTSITGPTTEIRALH 300
DB 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGITLCAKGCALDITGTSITGPTTEIRALH 300
QY 301 AAGGIPPLAGEYIILCSEIPKLPVSVFLGGVWFLNLTADHYVIQTTNRGVRCLCLSGFQA 360
DB 301 AAGGIPPLAGEYIILCSEIPKLPVSVFLGGVWFLNLTADHYVIQTTNRGVRCLCLSGFQA 360
QY 361 LDVPPAGFWILGDVFLGTVYAVFDRGDMKSSARVGLARARTRGADLGMGTAAQPPG 420
DB 350 -----DVFLGTVYAVFDRGDMKSSARVGLARARTRGADLGMGTAAQPPG 395

RESULT 6
US-09-387-413-3
; Sequence 3, Application US/09387413
; Patent No. 6475485
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; COLEMAN, Roger
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
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; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,413
; FILING DATE: 31-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/080,538
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0125 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT02
; CLONE: 312099
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-387-413-3

Query Match          92.5%; Score 2069.5; DB 4; Length 395;
Best Local Similarity 93.8%; Pred. No. 4.6e-205;
Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

QY 1 MSPPPQLQPLLLLLPLLNVPESGATLIRPLHRVQPGRRITNLLRGWREPAELPKLGAPS 60
DB 1 MSPPPQLQPLLLLLPLLNVPESGATLIRPLHRVQPGRRITNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNYRDVQVFEIGLTGTPQNFTVAEDTGSNNLWVPSRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNYRDVQVFEIGLTGTPQNFTVAEDTGSNNLWVPSRCHFFSVPCWLHH 120
QY 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPVSLVAF 180
DB 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSDKLTIGGIKASVIFGEALWEPVSLVAF 180
QY 181 AHFDGILGFPILSVEGVRRPMDVLEQGLLDKVPFSPYLNRPDEPDGGLVILGSDP 240
DB 181 AHFDGILGFPILSVEGVRRPMDVLEQGLLDKVPFSPYLNRPDEPDGGLVILGSDP 240
QY 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGITLCAKGCALDITGTSITGPTTEIRALH 300
DB 241 AHYIPPLTFVPTVPAYQIHMERYKVGPGITLCAKGCALDITGTSITGPTTEIRALH 300
QY 301 AAGGIPPLAGEYIILCSEIPKLPVSVFLGGVWFLNLTADHYVIQTTNRGVRCLCLSGFQA 360
DB 301 AAGGIPPLAGEYIILCSEIPKLPVSVFLGGVWFLNLTADHYVIQTTNRGVRCLCLSGFQA 360
QY 361 LDVPPAGFWILGDVFLGTVYAVFDRGDMKSSARVGLARARTRGADLGMGTAAQPPG 420
DB 350 -----DVFLGTVYAVFDRGDMKSSARVGLARARTRGADLGMGTAAQPPG 395

RESULT 7
US-08-974-691-6
```



```
; Sequence 6, Application US/08974691
; Patent No. 6225103
; GENERAL INFORMATION:
; APPLICANT: Keolsch, Gerald
; APPLICANT: Lin, Xinli
; APPLICANT: Tang, Jordan
; TITLE OF INVENTION: Cloning and Characterization of Napsin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; STREET: St.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,691
; FILING DATE: 20-NOV-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,196
; FILING DATE: 20-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,126
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP 166
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-974-691-6

Query Match 84.8%; Score 1897; DB 3; Length 445;
Best Local Similarity 86.0%; Pred. No. 3.5e-187;
Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

Qy 1 MSPPPLQLPLLLLPLLNVPESGATLIRPLHRVQPGRRRTLLRGRWREPAELPKLGAPS 60
Db 1 MSPPPLQLPLLLLPLLNVPESGATLIRPLHRVQPGRRRTLLRGRWREPAELPKLGAPS 60
Qy 61 PGDKPIFVLSNRYDVOYFGEIGLGTPTPQNTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPASVPSKFLDAQYFGEIGLGTPTPQNTVAFTDGTSSNLWVPSRRCHFFSVPCWFHH 120
Qy 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWESSLVFV 180
Db 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWESSLVFV 180
Qy 181 AHFGGILGLGPPILSVGVRPMDVLVEQGLLDPFVSFYLNRPDPDGGELVLGSDP 240
Db 181 SRPDGILGLGPPILSVGVRPMDVLVEQGLLDPFVSFYLNRPDPDGGELVLGSDP 240
Qy 241 AHYIPPLTFVPTVPAYQIHWERVKVGPGTLTCAKCAALTDGTSLITGPTTEIRALH 300
Db 241 AHYIPPLTFVPTVPAYQIHWERVKVGSRUTLCAQCAALTDGTSLITGPTTEIRALH 300

; Sequence 2, Application US/08974691
; Patent No. 6225103
; GENERAL INFORMATION:
; APPLICANT: Keolsch, Gerald
; APPLICANT: Lin, Xinli
; APPLICANT: Tang, Jordan
; TITLE OF INVENTION: Cloning and Characterization of Napsin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
; STREET: St.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,691
; FILING DATE: 20-NOV-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,196
; FILING DATE: 20-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,126
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP 166
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-974-691-2

Query Match 84.8%; Score 1897; DB 3; Length 451;
Best Local Similarity 86.0%; Pred. No. 3.6e-187;
Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

Qy 1 MSPPPLQLPLLLLPLLNVPESGATLIRPLHRVQPGRRRTLLRGRWREPAELPKLGAPS 60
Db 1 MSPPPLQLPLLLLPLLNVPESGATLIRPLHRVQPGRRRTLLRGRWREPAELPKLGAPS 60
Qy 61 PGDKPIFVLSNRYDVOYFGEIGLGTPTPQNTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPASVPSKFLDAQYFGEIGLGTPTPQNTVAFTDGTSSNLWVPSRRCHFFSVPCWFHH 120
Qy 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWESSLVFV 180
Db 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSEDKLTIGGKIGASVIFGEALWESSLVFV 180
Qy 181 AHFGGILGLGPPILSVGVRPMDVLVEQGLLDPFVSFYLNRPDPDGGELVLGSDP 240
Db 181 SRPDGILGLGPPILSVGVRPMDVLVEQGLLDPFVSFYLNRPDPDGGELVLGSDP 240
Qy 241 AHYIPPLTFVPTVPAYQIHWERVKVGPGTLTCAKCAALTDGTSLITGPTTEIRALH 300
Db 241 AHYIPPLTFVPTVPAYQIHWERVKVGSRUTLCAQCAALTDGTSLITGPTTEIRALH 300
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Db 121 RFPNASSKPSGTFKAIQYGTGRVGGILSSEKLTIGGKAGSVIFGEALWESSLVTV 180
QY 181 AHFDGILGLFPILSVEGVRPMDVLVEQGLDKPVSFYLNRPDPBGDELVLGGSDP 240
Db 181 SRPDGILGLFPILSVEGVRPMDVLVEQGLDKPVSFYFNRPDPBGDELVLGGSDP 240
QY 241 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTCAKGAALTDGTSLITGPTTEIRALH 300
Db 241 AHYIPPLTFVPTVPAYWQHMERVKVGSRTLCAQCAAILDTGTPVIVGPTTEIRALH 300
QY 301 AAGGIPLLAGEYIILCSEIPKLPAYSFLLGGVWFNLTAHDYVIQTTNRNGVRLCLSGFOA 360
Db 301 AAGGIPLLAGEYIIRCSKIPKLPAYSVLLIGGVWFNLTAQDYVIQFAQGDVRLCLSGFRA 360
QY 361 LDVPPGPFWILGDVFLGTVAVFDRGDMKSSARVGLARARTGADLGWGETAQAOFP 420
Db 361 LDIASPPVPVWILGDVFLGTVAVFDRGDMKSGARVGLARARPRGADLGRRETAQAQYRG 420

RESULT 9

US-09-705-448-3

; Sequence 3, Application US/09705448

; Patent No. 6432690

; GENERAL INFORMATION:

; APPLICANT: Xu, Hong

; APPLICANT: Bruno, Sandra A.

; APPLICANT: Elsenboss, Laura A.

; APPLICANT: Fogliano, Michael

; APPLICANT: Cohan, Victoria L.

; APPLICANT: Bandman, Olga

; TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES

; FILE REFERENCE: PF-0458-1 CIP

; CURRENT APPLICATION NUMBER: US/09/705,448

; CURRENT FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: 09/116,641

; PRIOR FILING DATE: 1998-07-16

; PRIOR APPLICATION NUMBER: 09/008,271

; PRIOR FILING DATE: 1998-01-16

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 433

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 322

; OTHER INFORMATION: 2435410, EOSINOT03

US-09-705-448-3

Query Match 83.9%; Score 1877; DB 4; Length 433;
Best Local Similarity 85.2%; Pred. No. 4e-185;
Matches 358; Conservative 17; Mismatches 45; Indels 0; Gaps 0;

QY 1 MSPPLLOPLLLPLLLNVEPSGATLIRIPHRVQPGRTNLLRGWREPAELPKLGAPS 60
Db 1 MSPPLLLPLLLPLNVEPAGATLIRIPHRVQPGRTNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNRYRDVQFGEIGLTPPONFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120
Db 61 PGDKPASPVLKFLDAQFGEIGLTPPONFTVAFTDGTSSNLWVPSRRCHFFSVPCWFHH 120
QY 121 RFDPKASSSQANGTKFAIQYGTGRVDGILSDKLTIGGKAGSVIFGEALWESSLVFAF 180
Db 121 RFPNASSKPSGTFKAIQYGTGRVDGILSDKLTIGGKAGSVIFGEALWESSLVFAF 180
QY 181 AHFDGILGLFPILSVEGVRPMDVLVEQGLDKPVSFYLNRPDPBGDELVLGGSDP 240
Db 181 SRPDGILGLFPILSVEGVRPMDVLVEQGLDKPVSFYFNRPDPBGDELVLGGSDP 240
QY 241 AHYIPPLTFVPTVPAYWQHMERVKVGPGLTCAKGAALTDGTSLITGPTTEIRALH 300

Db 241 AHYIPPLTFVPTVPAYWQHMERVKVGSRTLCAQCAAILDTGTPVIVGPTTEIRALH 300
QY 301 AAGGIPLLAGEYIILCSEIPKLPAYSFLLGGVWFNLTAHDYVIQTTNRNGVRLCLSGFOA 360
Db 301 AAGGIPLLAGEYIIRCSKIPKLPAYSVLLIGGVWFNLTAQDYVIQFAQGDVRLCLSGFRA 360
QY 361 LDVPPGPFWILGDVFLGTVAVFDRGDMKSSARVGLARARTGADLGWGETAQAOFP 420
Db 361 LDIASPPVPVWILGDVFLGTVAVFDRGDMKSGARVGLARARPRGADLGRRETAQAQYRG 420

RESULT 10

US-08-974-691-3

; Sequence 3, Application US/08974691

; Patent No. 6225103

; GENERAL INFORMATION:

; APPLICANT: Keolsch, Gerald

; APPLICANT: Lin, Xinli

; APPLICANT: Tang, Jordan

; TITLE OF INVENTION: Cloning and Characterization of Napsin

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center, 1201 W. Peachtree

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,691

; FILING DATE: 20-NOV-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/031,196

; FILING DATE: 20-NOV-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/046,126

; FILING DATE: 09-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: OMRF 166

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404-873-8794

; TELEFAX: 404-873-8795

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 419 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-974-691-3

Query Match 69.9%; Score 1564.5; DB 3; Length 419;
Best Local Similarity 70.5%; Pred. No. 6.8e-153;
Matches 297; Conservative 36; Mismatches 79; Indels 9; Gaps 3;

QY 7 LQPIILLPLL---NVPSGATLIRIPHRVQPGRTNLLRGWREPAELPKLGAPSGD 63
Db 1 MSPLLLLCLLGNLEPEAKLRVPLQRIHLGRIILNPLNGWEQLAELSR--TSTSGG 58
QY 64 KPIFVPLSNRYRDVQFGEIGLTPPONFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHHRFD 123
Db 59 NPSFVPLSKFWNTQYFGTIGLTPPONFTVAFTDGTSSNLWVPSRRCHFFSLACWFHFRFN 118
QY 124 PRASSSQANGTKFAIQYGTGRVDGILSDKLTIGGKAGSVIFGEALWESSLVFAFAHF 183

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119 PKASSFRPMGKFAIQYGTGRSLGSLSDNLFIGGHDFAVTFGEALWEPSLIFALAHF 178
184 DGILGLGFPILSVGVRPPMDVLVEQGLDKPVFSFYLNDRDPEPGGELVLGGSDPAHY 243
179 DGILGLGFPFLAVGGVQPPLDAMVEQGLLEKPVFSFYLNDRDSEGGELVLGGSDPAHY 238
244 IPPLTFVPTVPAYWQIHMVRKVGGLTLCAGCAAILDTGSLITGPTTEIRALHAAI 303
239 VPPLTFIPVTIPAYWQVHMESVKVGTGLSLCAQCSAILDTGSLITGPTSEIRALNKAI 298
304 GGIIPLAGYIILCSBIPKLPVAVFLLGGVWFLTAHDYVIQTRNGVRLCLSGFOALDV 363
299 GGYFPLNGQYFIQCSKTPTLPVPSFHLGGVWFLTGQDYVIQDLSGVDGLCLGFOALDI 358
364 PPAGPFWILGDVFLGYVAVFDRGDMKSSARVGLARTRGADLWGGETAQOAF---P 419
359 PKPAGPFWILGDVFLGYVAVFDRGDMKSSARVGLARTRGADLWGGETAQOAF---P 418
420 G 420
419 G 419

```

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RESULT 11
US-09-705-448-10
; Sequence 10, Application US/09705448
; Patent No. 6432690
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Bruno, Sandra A.
; APPLICANT: Elsenboss, Laura A.
; APPLICANT: Fogliano, Michael
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES
; FILE REFERENCE: PF-0458-1 CIP
; CURRENT APPLICATION NUMBER: US/09/705,448
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/116,641
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/008,271
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 419
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
; FEATURE:
; OTHER INFORMATION: 1906810, GenBank
US-09-705-448-10

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```

Query Match 69.7%; Score 1560.5; DB 4; Length 419;
Best Local Similarity 70.3%; Pred. No. 1.8e-152;
Matches 296; Conservative 37; Mismatches 79; Indels 9; Gaps 3;

7 LQPLLLLLPL--NVPSGATLRIRPLRVQGRRTLNLLRGWREPAELPKLGAPSGD 63
1 MSPILLLLCLLNLGNEPEERAKLRVPLQRIHLGRLINPLNGWEQLAELSR--TSTSG 58

64 KPFIPLSNTRDVQYFGEIGLGTTPQNTFAVDTGSSNLWVPSRRCHFFSPVCLHHRFD 123
59 NPSEVPLSKFMTQYFGTIGLGTTPQNTFAVDTGSSNLWVPSRRCHFFSLACWFHFRN 118

124 PKASSSQANGTKFAIQYGTGRVDCGLISDGLTGGIKGASVIFGEALWEPSLIFALAHF 183
119 PKASSSRPNKTKFAIQYGTGRSLGSLSDNLFIGGHDFAVTFGEALWEPSLIFALAHF 178
184 DGILGLGFPILSVGVRPPMDVLVEQGLDKPVFSFYLNDRDPEPGGELVLGGSDPAHY 243
179 DGILGLGFPFLAVGGVQPPLDAMVEQGLLEKPVFSFYLNDRDSEGGELVLGGSDPAHY 238

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244 IPPLTFVPTVPAYWQIHMVRKVGGLTLCAGCAAILDTGSLITGPTTEIRALHAAI 303
239 VPPLTFIPVTIPAYWQVHMESVKVGTGLSLCAQCSAILDTGSLITGPTSEIRALNKAI 298
304 GGIIPLAGYIILCSBIPKLPVAVFLLGGVWFLTAHDYVIQTRNGVRLCLSGFOALDV 363
299 GGYFPLNGQYFIQCSKTPTLPVPSFHLGGVWFLTGQDYVIQDLSGVDGLCLGFOALDI 358
364 PPAGPFWILGDVFLGYVAVFDRGDMKSSARVGLARTRGADLWGGETAQOAF---P 419
359 PKPAGPFWILGDVFLGYVAVFDRGDMKSSARVGLARTRGADLWGGETAQOAF---P 418
420 G 420
419 G 419

RESULT 12
US-08-208-007A-12
; Sequence 12, Application US/08208007A
; Patent No. 5501969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, ET AL.
; TITLE OF INVENTION: Human Osteoclast-Derived Cathepsin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,007A
; FILING DATE: March 8, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5501969e
; FILING DATE: No. 5501969e
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-007A-12

```

```

Query Match 45.4%; Score 1015; DB 1; Length 412;
Best Local Similarity 46.9%; Pred. No. 3.5e-96;
Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

1 MSPPLIQLPLLLPLINVEPSGATLRIRPLRVQGRRTLNLLRGWRE-----PAELP 54
1 MQPSLLPLALCLL----AAPASA-LVRPLHLKFTSIRRTMSEVGGSVEDLIAKGPVSKY 55

55 KLGAAPSQDKPIFVPLSNTRDVQYFGEIGLGTTPQNTFAVDTGSSNLWVPSRRCHFFSV 114
56 SQAVPAVTEGPIEVLKNYMDAQYIGEIGLGTTPQNTFAVDTGSSNLWVPSHCKLIDI 115

```

Qy 115 PCWLHHRFDPKASSFOANGTKFAIQTGTRVDGILSDKLT1-----GGIKGA 163
 Db 116 ACWIHHKNSDKSTYVKNKTSFIDHYGSGSLGYLSQDTSVPCQSASSASALGGYKVE 175
 Qy 164 SVIFGEALWEPSSLVFAFAHFDGILGLGPILSVGVPRPMDVLVEQGLLDKPFVSFYLR 223
 Db 176 RQVFEATKPGITFAIAKFDGILGMAYPRISVNNVLPVFDNLMOQKLVQDNIFSFYLSR 235
 Qy 224 DPBEPDGGELVGGSDPAHYIPPLTFVPTVPYQWQHMERVKYGPGLTLCCKAAILD 283
 Db 236 DPDAQPGGELMLGGTDSKYKGSLSYLVNTRKAYQVHLDQVEVASGLTLCCKECEAIVD 295
 Qy 284 TGTSLITGPTTEIRALHAAIGGIPILAGEYIILCSEIPKLPKPAVSLGGVWFLNLTADYV 343
 Db 296 TGTSLMVGPVDEVELQKGAIVPLIQEYMIPEKVKSTLPAITLKLGGKGYKLSPEYDT 355
 Qy 344 IOTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTVAVFDGDMKSSARVGLARA 401
 Db 356 LKVSQAGKTLCLSGFMGMDIPPPSGPLWILGDVFIGRYTYTFDR-----DNNRVGFAEA 409

RESULT 13

US-08-974-691-4
 ; Sequence 4, Application US/08974691
 ; Patent No. 6225103
 ; GENERAL INFORMATION:
 ; APPLICANT: Keolsch, Gerald
 ; APPLICANT: Lin, Xinli
 ; APPLICANT: Tang, Jordan
 ; TITLE OF INVENTION: Cloning and Characterization of Napsin
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center, 1201 W. Peachtree
 ; CITY: Atlanta
 ; STATE: GA
 ; COUNTRY: USA
 ; ZIP: 30309-3450
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,691
 ; FILING DATE: 20-NOV-1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/031,196
 ; FILING DATE: 20-NOV-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/046,126
 ; FILING DATE: 09-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: OMR# 166
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-873-8794
 ; TELEFAX: 404-873-8795
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 412 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-08-974-691-4

Query Match 45.4%; Score 1015; DB 3; Length 412;

Best Local Similarity 46.9%; Pred. No. 3.5e-96;
 Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;
 Qy 1 MSPPPLLOPILLLPLLNVPSPGATLIRIPHRVQPGRRITNLLRGWRE-----PAELP 54
 Db 1 MQPSSLLPLALCLL-----AAPASA-LVRIPLHKFTSIRRTMSEVGGSVEDLIAKGPVSKY 55
 Qy 55 KLGAPSPGDKPIFVPLSNYRDVQVFGIEGLGTPPQNFVAFDTGSSNLWVPSRRCHPFSV 114
 Db 56 SQAVPATEGPPIEVLLKNYMDAQYGEIGIGITPPQCTVVFDTGSSNLWVPSIHKLLDI 115
 Qy 115 PCWLHHRFDPKASSFOANGTKFAIQTGTRVDGILSDKLT1-----GGIKGA 163
 Db 116 ACWIHHKNSDKSTYVKNKTSFIDHYGSGSLGYLSQDTSVPCQSASSASALGGYKVE 175
 Qy 164 SVIFGEALWEPSSLVFAFAHFDGILGLGPILSVGVPRPMDVLVEQGLLDKPFVSFYLR 223
 Db 176 RQVFEATKPGITFAIAKFDGILGMAYPRISVNNVLPVFDNLMOQKLVQDNIFSFYLSR 235
 Qy 224 DPBEPDGGELVGGSDPAHYIPPLTFVPTVPYQWQHMERVKYGPGLTLCCKAAILD 283
 Db 236 DPDAQPGGELMLGGTDSKYKGSLSYLVNTRKAYQVHLDQVEVASGLTLCCKECEAIVD 295
 Qy 284 TGTSLITGPTTEIRALHAAIGGIPILAGEYIILCSEIPKLPKPAVSLGGVWFLNLTADYV 343
 Db 296 TGTSLMVGPVDEVELQKGAIVPLIQEYMIPEKVKSTLPAITLKLGGKGYKLSPEYDT 355
 Qy 344 IOTTRNGVRLCLSGFQALDVPDPAGPFWILGDVFLGTVAVFDGDMKSSARVGLARA 401
 Db 356 LKVSQAGKTLCLSGFMGMDIPPPSGPLWILGDVFIGRYTYTFDR-----DNNRVGFAEA 409

RESULT 14

US-08-915-095A-12
 ; Sequence 12, Application US/08915095A
 ; Patent No. 6383793
 ; GENERAL INFORMATION:
 ; APPLICANT: Hastings, et al.
 ; TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHEPSIN
 ; FILE REFERENCE: PF107D4
 ; CURRENT APPLICATION NUMBER: US/08/915,095A
 ; CURRENT FILING DATE: 1997-08-20
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 412
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-915-095A-12

Query Match 45.4%; Score 1015; DB 4; Length 412;
 Best Local Similarity 46.9%; Pred. No. 3.5e-96;
 Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;
 Qy 1 MSPPPLLOPILLLPLLNVPSPGATLIRIPHRVQPGRRITNLLRGWRE-----PAELP 54
 Db 1 MQPSSLLPLALCLL-----AAPASA-LVRIPLHKFTSIRRTMSEVGGSVEDLIAKGPVSKY 55
 Qy 55 KLGAPSPGDKPIFVPLSNYRDVQVFGIEGLGTPPQNFVAFDTGSSNLWVPSRRCHPFSV 114
 Db 56 SQAVPATEGPPIEVLLKNYMDAQYGEIGIGITPPQCTVVFDTGSSNLWVPSIHKLLDI 115
 Qy 115 PCWLHHRFDPKASSFOANGTKFAIQTGTRVDGILSDKLT1-----GGIKGA 163
 Db 116 ACWIHHKNSDKSTYVKNKTSFIDHYGSGSLGYLSQDTSVPCQSASSASALGGYKVE 175
 Qy 164 SVIFGEALWEPSSLVFAFAHFDGILGLGPILSVGVPRPMDVLVEQGLLDKPFVSFYLR 223
 Db 176 RQVFEATKPGITFAIAKFDGILGMAYPRISVNNVLPVFDNLMOQKLVQDNIFSFYLSR 235
 Qy 224 DPBEPDGGELVGGSDPAHYIPPLTFVPTVPYQWQHMERVKYGPGLTLCCKAAILD 283
 Db 236 DPDAQPGGELMLGGTDSKYKGSLSYLVNTRKAYQVHLDQVEVASGLTLCCKECEAIVD 295

```
QY 284 TGTSLTGPTBEIRALHAAIGGIPLLAGEYIILCSEIPKLPVSVFLGGVWFNLTAHDYV 343
Db 296 TGTSLSWGPVDEVELQKAGVLIQGEYMWPCVKSTLPAITIKLGKGYKLSPEDYT 355
QY 344 IQTTRNGVRLCLSGFQALDVPFPAGPWILGDVFLGTGYVAVFDRGDMKSSARVGLARA 401
Db 356 LKVSQAGKTLCLSGFMGMNDIPPPSGPLWILGDVFIGRYTYTVFDR----DNNRVGFAEA 409

RESULT 15
US-08-798-096-12
; Sequence 12, Application US/08798096
; Patent No. 6387682
; GENERAL INFORMATION:
; APPLICANT: Hastings, et al.
; TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHEPSIN
; FILE REFERENCE: PF107D2
; CURRENT APPLICATION NUMBER: US/08/798,096
; CURRENT FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-798-096-12

Query Match 45.4%; Score 1015; DB 4; Length 412;
Best Local Similarity 46.9%; Pred. No. 3.5e-96;
Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

QY 1 MSPPLLOPLLPLLLPLLNVPESGATLIRIPLHRVQPCERTLNLLRGWRE-----PAELP 54
Db 1 MQPSLLPLALCLL-----AAPASA-LVRIPLHKFTSIRRTMSEVGSVEDLIAKGPVSKY 55
QY 55 KLGAPSPGDKPIFVPLSNYRDVQYFGEIGLGTPTPQNFVAFDTGSSNLWVPSRCHFFSV 114
Db 56 SQAVPAVTEGPIPEVLKNYMDAQYVYGEIGTGPQCFTVVFDTGSSNLWVPSIHCKLLDI 115
QY 115 PCWLHHRFPDKASSPQANGTKFAIQYGTGRVDGILSEDKLT-----GGIKGA 163
Db 116 ACWTHHKYNSDKSTYVKNGTGTFDIHYGSSGLSGYLSQDTVSPCQSASSASALGGVKVE 175
QY 164 SVIFGEALWEPSLVFAFAHFDGILGFPILSVGVRRPMDVLVEQGLDKPVFSFYLN 223
Db 176 RQVGEATKQGITFIAAKFDGILGMAYPRISVNNVLVFDNLMOQLVDQNIFFYLSR 235
QY 224 DPEEPDGGELVLGSDPAHYIPPLTFVPVTPYAWQIHMERVKVGPGLTLCAKCAAILD 283
Db 236 DPDAQPGGELMLGGTDSKYKYSYLNVTNRKAYQVHLQDQEVASGLTLCKEGCEAIVD 295
QY 284 TGTSLTGPTBEIRALHAAIGGIPLLAGEYIILCSEIPKLPVSVFLGGVWFNLTAHDYV 343
Db 296 TGTSLSWGPVDEVELQKAGVLIQGEYMWPCVKSTLPAITIKLGKGYKLSPEDYT 355
QY 344 IQTTRNGVRLCLSGFQALDVPFPAGPWILGDVFLGTGYVAVFDRGDMKSSARVGLARA 401
Db 356 LKVSQAGKTLCLSGFMGMNDIPPPSGPLWILGDVFIGRYTYTVFDR----DNNRVGFAEA 409
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Search completed: June 2, 2004, 20:23:16
Job time : 30.2707 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 19:59:24 ; Search time 100.065 Seconds
(without alignments)
1185.931 Million cell updates/sec

Title: US-09-700-770-8
 Perfect score: 2238
 Sequence: 1 MSEPPLQLQLLLLLPLLNVE.....ARTRGADLWGGETAQAQFPG 420

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :
A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
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SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2238	100.0	420	2	AAV06435	AAV06435	Human pro
2	2238	100.0	420	3	AAV44809	AAV44809	Human Asp
3	2238	100.0	420	3	AAV44457	AAV44457	Human lun
4	2232	99.7	420	2	AAW54878	AAW54878	Human nap
5	2232	99.7	420	6	AAE37358	AAE37358	Human nap
6	2232	99.7	433	5	AAO20497	AAO20497	Protein o
7	2069.5	92.5	395	2	AAW37958	AAW37958	Amino aci
8	1897	84.8	438	2	AAW57042	AAW57042	Human asp
9	1897	84.8	451	2	AAW54877	AAW54877	Human nap
10	1887	84.3	433	3	AAV44810	AAV44810	Human Asp
11	1702.5	76.1	390	4	AAU09094	AAU09094	Novel hum
12	1678.5	75.0	449	2	AAW57043	AAW57043	Human asp
13	1560.5	69.7	419	3	AAV79177	AAV79177	Haematopo
14	1343	60.0	288	4	AAU23066	AAU23066	Human hum
15	1328	59.3	262	4	AAAB85539	AAAB85539	Human sec
16	1328	59.3	262	5	ABG76585	ABG76585	Human sec
17	1328	59.3	262	5	ABG64720	ABG64720	Human alb
18	1179	52.7	285	3	AAAB58332	AAAB58332	Lung canc
19	1050	46.9	212	4	AAAB85560	AAAB85560	Human sec
20	1050	46.9	212	5	ABG76606	ABG76606	Human sec
21	1050	46.9	212	5	ABG64722	ABG64722	Human alb
22	1037	46.3	410	4	AAE01672	AAE01672	Human gen
23	1037	46.3	410	5	ABG63963	ABG63963	Human alb
24	1037	46.3	410	6	ADA57122	ADA57122	Human sec
25	1037	46.3	410	6	ADA40983	ADA40983	Human sec

ALIGNMENTS

RESULT 1

AA06435
ID AAY06435 standard; protein; 420 AA.

```

XX PD 22-JUL-1999.
XX PF 12-JAN-1999; 99WO-US000655.
XX PR 16-JAN-1998; 98US-00008271.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Bandman O, Hillman JL, Yue H, Guegler KJ, Corley NC, Tang YT;
XX PI Shah P;
XX WPI: 1999-430616/36.
XX DR N-PSDB; AAX87152.
XX PT Novel human protease molecules useful in the treatment of developmental
XX PT disorders and/or cancers.
XX PS Claim 1; Page 72-73; 90pp; English.
XX CC The present sequence represents novel human protease HUPM-4, as deduced
XX CC from the consensus sequence (see AAX87152) of overlapping cDNA clones
XX CC obtained from various libraries. Northern analysis shows expression of
XX CC HUPM-4 in cardiovascular, haematopoietic, and male and female
XX CC reproductive cDNA libraries. Approximately 56% of these libraries are
XX CC associated with neoplastic disorders, 18% with inflammation and the
XX CC immune response, and 18% with trauma. The invention provides 12 new human
XX CC proteases, i.e. HUPM-1 to -12 (see AAY06432-43), and the polynucleotides
XX CC encoding them (see AAX87149-60). Also provided are vectors, host cells
XX CC and methods for producing HUPM polypeptides, as well as agonists and
XX CC antagonists of HUPM. Methods for treating or preventing cell
XX CC proliferative disorders and immune disorders using HUPM or HUPM
XX CC antagonists are claimed
XX SQ Sequence 420 AA;
    Query Match 100.0%; Score 2238; DB 2; Length 420;
    Best Local Similarity 100.0%; Pred No. 6.9e-203;
    Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQGRRTNLLRGWRPAPLKLIGAPS 60
DB 1 MSPPPLQLPLLLLPLLNVEPSGATLIRPLHRVQGRRTNLLRGWRPAPLKLIGAPS 60
QY 61 PGDKPIFVPLSNRYDVQYGEIGLGPONFTVAEDTSSNLWVPSRCHFFSVPCWLHH 120
DB 61 PGDKPIFVPLSNRYDVQYGEIGLGPONFTVAEDTSSNLWVPSRCHFFSVPCWLHH 120
QY 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEP SILVFAF 180
DB 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEP SILVFAF 180
QY 181 AHFDGILGLGFPILSVEGVRPMDVLVEOGLLDKPVFSYLNDRDPDPGGELVLGGSDP 240
DB 181 AHFDGILGLGFPILSVEGVRPMDVLVEOGLLDKPVFSYLNDRDPDPGGELVLGGSDP 240
QY 241 AHYIPPLTFVPVTVBAYWQIHMERVKVGPGLTICAKGCAAILDTGSLTGTPEETRALH 300
DB 241 AHYIPPLTFVPVTVBAYWQIHMERVKVGPGLTICAKGCAAILDTGSLTGTPEETRALH 300
QY 301 AAIIGIPLLAGIYIILCSEIKPLPAVSFLGGVWFNLTAHDYVIQTRNGVRLCLSGFQA 360
DB 301 AAIIGIPLLAGIYIILCSEIKPLPAVSFLGGVWFNLTAHDYVIQTRNGVRLCLSGFQA 360
QY 361 LDVPPAGPFWIIGDVFLGTVAVFDRGDMKSSARVGLARPARTRGADLWGETAQOQFPG 420
DB 361 LDVPPAGPFWIIGDVFLGTVAVFDRGDMKSSARVGLARPARTRGADLWGETAQOQFPG 420

```

RESULT 2

AAY44809

ID AAY44809 standard; protein; 420 AA.

XX

```

AC AAY44809;
XX 18-MAY-2000 (first entry)
XX Human Aspartic Protease-1 (NHAP-1).
XX Human; aspartic protease-1; NHAP-1; chromosome 19q13.3; antiallergic;
XX immunosuppressive; cytostatic; antiasthmatic; antiinflammatory; cancer;
XX antiarteriosclerotic; antithyroid; antibacterial; neuroprotective;
XX antidiabetic; anti-HIV; osteopathic; antiarthritic; treatment; cretinism;
XX endocrinological; hypogonadism; Sheehan syndrome; diabetes insipidus;
XX hypothyroidism; adenocarcinoma; leukaemia; immunological; amyloidosis;
XX acquired immune deficiency syndrome; AIDS; Addison's disease; arthritis;
XX osteoporosis; atherosclerosis; infection; respiratory; allergy; asthma;
XX emphysema; gene therapy; diagnosis.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Pep-side 1..21
XX /label= Signal_peptide
XX /note= "Potential"
XX Protein 22..420
XX /label= Mature_NHAP-1
XX /note= "Homologous to mouse aspartic protease-like
XX protein (GI 1906810)"
XX Modified-site 60
XX /note= "potential casein kinase II phosphorylation site"
XX Modified-site 90
XX /note= "Potential N-glycosylation site"
XX Active-site 96
XX /note= "Potential active site Asp residue characteristic
XX of aspartic proteases"
XX Modified-site 106
XX /note= "Potential protein kinase C phosphorylation site"
XX Modified-site 133
XX /note= "Potential N-glycosylation site"
XX Modified-site 143
XX /note= "Potential protein kinase C phosphorylation site"
XX Active-site 283
XX /note= "Potential active site Asp residue characteristic
XX of aspartic proteases"
XX Misc-difference 309
XX /note= "Potential Leucine zipper pattern start site"
XX Misc-difference 316
XX /note= "Potential Leucine zipper pattern start site"
XX Modified-site 336
XX /note= "Potential N-glycosylation site"
XX Modified-site 338
XX /note= "Potential casein kinase II phosphorylation site"
XX Modified-site 346
XX /note= "Potential protein kinase C phosphorylation site"
XX Binding-site 387..389
XX /note= "Potential cell attachment site"
XX Modified-site 393
XX /note= "Potential protein kinase C phosphorylation site"
XX WO200004137-A1.
XX 27-JAN-2000.
XX 15-JUL-1999; 99WO-US015988.
XX 16-JUL-1998; 98US-00116641.
XX (INCY-) INCYTE PHARM INC.
XX Xu H, Bruno SA, Eelsenboss LA, Fogliano M, Cohan VL, Bandman O;
XX WPI: 2000-182413/16.
XX N-PSDB; AAX50231.
XX New human aspartic protease polypeptide useful for treating and detecting

```

PT endocrinological disorders e.g. hypogonadism, Sheehan syndrome and
 XX diabetes insipidus.
 XX
 PS Disclosure; Fig 1; 83pp; English.
 XX
 CC The present sequence is human aspartic protease-1 (NHAP-1) encoded by
 CC cDNA obtained from human lung cDNA library. NHAP-1 gene is located on
 CC chromosome 19q13.3. NHAP has immunosuppressive, antiallergic, cytostatic,
 CC antiasthmatic, antiinflammatory, antiarteriosclerotic, antithyroid,
 CC antibacterial, neuroprotective, antidiabetic, anti-HIV, osteopathic and
 CC antiarthritic activity. It is useful for treating and preventing
 CC endocrinological disorders like hypogonadism, Sheehan syndrome, diabetes
 CC insipidus, cretinism and hypothyroidism, cancers like adenocarcinoma and
 CC leukaemia, immunological disorders like acquired immune deficiency
 CC syndrome (AIDS), Addison's disease, amyloidosis, arthritis, osteoporosis,
 CC atherosclerosis and microbial infections and respiratory disorders like
 CC allergy, asthma and emphysema. NHAP polynucleotides can be used in gene
 CC therapy and for diagnosis of disorders associated with expression of NHAP
 XX
 SQ Sequence 420 AA;
 Query Match 100.0%; Score 2238; DB 3; Length 420;
 Best Local Similarity 100.0%; Pred. No. 6.9e-203;
 Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSPPPPLQLLLLLPLLNVPSPGATLIRIPLHRVQPGRTINLLRGWREPAELPKLGAPS 60
 DB 1 MSPPPPLQLLLLLPLLNVPSPGATLIRIPLHRVQPGRTINLLRGWREPAELPKLGAPS 60
 QY 61 PGDKPIFVPLSNRVDVQYFGEIGLGTTPQNTFAFTGSSNLMWPSRRCHFFSVPCWLHH 120
 DB 61 PGDKPIFVPLSNRVDVQYFGEIGLGTTPQNTFAFTGSSNLMWPSRRCHFFSVPCWLHH 120
 QY 121 RFPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPFLVFAF 180
 DB 121 RFPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPFLVFAF 180
 QY 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLLDKPFVSYLNRPDPDPDGELVLGSDP 240
 DB 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLLDKPFVSYLNRPDPDPDGELVLGSDP 240
 QY 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTLCAGCAAILDTGSLITGPTTEIRALH 300
 DB 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTLCAGCAAILDTGSLITGPTTEIRALH 300
 QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTAHDYVIQTRNGVRLCLSGFOA 360
 DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTAHDYVIQTRNGVRLCLSGFOA 360
 QY 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTGADLGMGETAQAOFPFG 420
 DB 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTGADLGMGETAQAOFPFG 420
 RESULT 3
 AAY44457
 ID AAY44457 standard; protein; 420 AA.
 XX
 AC AAY44457;
 XX
 XX 27-MAR-2000 (first entry)
 XX
 XX Human lung specific gene protein Lngl105.
 XX
 XX Lung Specific Gene; LSG; Lngl105; human; diagnostic marker; prognosticate;
 XX lung cancer; diagnosis.
 XX
 XX Homo sapiens.
 XX
 XX WO9960160-A1.
 XX
 XX 25-NOV-1999.
 XX
 XX

PF 12-MAY-1999; 99WO-US010344.
 XX
 PR 21-MAY-1998; 98US-0086212P.
 XX
 PA (DIAD-) DIADEXUS LLC.
 XX
 XX Yang F, Macina RA, Sun Y;
 XX WPI; 2000-116320/10.
 DR N-PSDB; AAZ29722.
 XX
 PT A new method for diagnosing, monitoring and staging lung cancer.
 XX
 XX Example 2; Page 37-38; 40pp; English.
 XX
 CC The present sequence is a lung specific gene (LSG) protein Lngl105 from
 CC human clone ID 3107312. The LSG has high level of tissue specificity for
 CC lungs and is overexpressed in cancerous tissues. The sequence serves as a
 CC diagnostic marker for detecting, monitoring, staging and prognosticating
 CC lung cancer. The diagnosis involves comparing levels of LSG in samples
 CC obtained from patient and normal control
 XX
 SQ Sequence 420 AA;
 Query Match 100.0%; Score 2238; DB 3; Length 420;
 Best Local Similarity 100.0%; Pred. No. 6.9e-203;
 Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSPPPPLQLLLLLPLLNVPSPGATLIRIPLHRVQPGRTINLLRGWREPAELPKLGAPS 60
 DB 1 MSPPPPLQLLLLLPLLNVPSPGATLIRIPLHRVQPGRTINLLRGWREPAELPKLGAPS 60
 QY 61 PGDKPIFVPLSNRVDVQYFGEIGLGTTPQNTFAFTGSSNLMWPSRRCHFFSVPCWLHH 120
 DB 61 PGDKPIFVPLSNRVDVQYFGEIGLGTTPQNTFAFTGSSNLMWPSRRCHFFSVPCWLHH 120
 QY 121 RFPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPFLVFAF 180
 DB 121 RFPKASSSQFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPFLVFAF 180
 QY 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLLDKPFVSYLNRPDPDPDGELVLGSDP 240
 DB 181 AHFDGILGLGFPILSVGVRPPMDVLVEQGLLDKPFVSYLNRPDPDPDGELVLGSDP 240
 QY 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTLCAGCAAILDTGSLITGPTTEIRALH 300
 DB 241 AHYIPPLTFVPTVPAYWQIHMERVKVGPGLTLCAGCAAILDTGSLITGPTTEIRALH 300
 QY 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTAHDYVIQTRNGVRLCLSGFOA 360
 DB 301 AAIGGIPLLAGEYIILCSEIPKLPVAVSFLGGVWFNLTAHDYVIQTRNGVRLCLSGFOA 360
 QY 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTGADLGMGETAQAOFPFG 420
 DB 361 LDVPPPPAGPFWILGDVFLGTYYAVFDRGDMKSSARVGLARARTGADLGMGETAQAOFPFG 420
 RESULT 4
 AAW54878
 ID AAW54878 standard; protein; 420 AA.
 XX
 AC AAW54878;
 XX
 XX 26-CCT-1998 (first entry)
 XX
 XX Human napsin B protein.
 XX
 XX Napsin B; splicing; clone; screening; human liver cDNA library;
 XX aspartic protease; N-terminal; C-terminal; genomic clone; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO9822597-A2.
 XX
 XX

XX 28-MAY-1998.
 XX 20-NOV-1997; 97WO-US021694.
 XX 20-NOV-1996; 96US-0031196P.
 XX 09-MAY-1997; 97US-0046126P.
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 XX Keolsch G, Lin X, Tang JUN;
 XX WPI; 1998-312482/27.
 XX N-PSDB; AAV27038.
 XX
 XX New isolated aspartic protease, napsin, from human liver - potentially
 XX useful for, e.g. diagnosis and treatment of disease.
 XX
 XX Disclosure; Fig 4; 24pp; English.
 XX
 XX The present sequence represents the human napsin B protein, encoded by
 XX the cDNA sequence given in AAV27038. The N-terminus of this cDNA was
 XX obtained by splicing together isolated napsin cDNA clones, which had been
 XX found by screening a human liver cDNA library, whereas the C-terminus was
 XX obtained by using genomic clones. Napsin B is an aspartic protease which
 XX was isolated from human liver
 XX
 XX Sequence 420 AA;

Query Match 99.7%; Score 2232; DB 2; Length 420;
 Best Local Similarity 99.8%; Pred. No. 2.6e-202;
 Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSPPPPLQPLLLPLLNVEPSGATLIRPLHRVQPGRTILRLRGWRPAPLPLKLGAPS 60
 Db 1 MSPPPPLQPLLLPLLNVEPSGATLIRPLHRVQPGRTILRLRGWRPAPLPLKLGAPS 60
 QY 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120
 Db 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120
 QY 121 REDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAP 180
 Db 121 REDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAP 180
 QY 181 AHFDGILGLGFPILSVGEVRPMDVLVEQGLLDKPVFSFVLNDRDPEDGGELVLGSDP 240
 Db 181 AHFDGILGLGFPILSVGEVRPMDVLVEQGLLDKPVFSFVLNDRDPEDGGELVLGSDP 240
 QY 241 AHYIPPLTFVTPVAYWQIHMERVKVGPGLTLCANGCAAILDTGTSLLITGPTTEIRALH 300
 Db 241 AHYIPPLTFVTPVAYWQIHMERVKVGPGLTLCANGCAAILDTGTSLLITGPTTEIRALH 300
 QY 301 AATGGIPLLAGEVILLCSIEPKLPVASFLLGGVWFNLTAHDYVIOTRNGVRLCLSGFOA 360
 Db 301 AATGGIPLLAGEVILLCSIEPKLPVASFLLGGVWFNLTAHDYVIOTRNGVRLCLSGFOA 360
 QY 361 LDVPPAGPFWIIGDVLGTVVAFVDRGDMKSSARVGLARTRGADLNGETAGQAQFP 420
 Db 361 LDVPPAGPFWIIGDVLGTVVAFVDRGDMKSSARVGLARTRGADLNGETAGQAQFP 420

RESULT 5
 AAE37358
 ID AAE37358 standard; protein; 420 AA.
 XX
 XX AAE37358;
 AC
 XX 27-AUG-2003 (first entry)
 DT
 XX Human napsin A, 93804 protein.
 DE
 XX Human; cardiovascular disorder; coronary artery disease; bradycardia;

KW restenosis; cardiac hypertrophy; ischaemia reperfusion injury; angina;
 KW arteriosclerosis; coronary artery ligation; rheumatic heart disease;
 KW heart failure; hypertension; cardiomyopathy; myocardial infarction;
 KW arterial inflammation; microembolism; atherosclerosis; endocarditis;
 KW vascular heart disease; valvular disease; arrhythmia; gene therapy;
 XX sinus node dysfunction; napsin A.
 XX Homo sapiens.
 XX WO2003039341-A2.
 XX 15-MAY-2003.
 XX 05-NOV-2002; 2002WO-US035538.
 XX 05-NOV-2001; 2001US-0339582P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Logan TJ, Chun M, Galvin KM;
 XX WPI; 2003-441437/41.
 XX N-PSDB; AAD56525.
 XX
 XX Treating a subject having a cardiovascular disorder, e.g. angina,
 XX arrhythmia, or restenosis, comprises administering a 139, 258, 1261,
 XX 1486, 2398, 2414, 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or
 XX 93804 modulator.

Disclosure; Page 123-124; 124pp; English.
 XX
 XX The invention relates to methods and compositions for treating a subject
 XX having a cardiovascular disorder using 139, 258, 1261, 1486, 2398, 2414,
 XX 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or 93804 modulator.
 XX The invention is useful for treating a cardiovascular disorder, including
 XX arteriosclerosis, atherosclerosis, vascular wall remodeling, restenosis,
 XX cardiac hypertrophy, ischaemia reperfusion injury, arterial inflammation,
 XX ventricular remodeling, rapid ventricular pacing, tachycardia, coronary
 XX microembolism, bradycardia, pressure overload, aortic bending, coronary
 XX artery ligation, valvular heart disease, valvular disease, including but
 XX not limited to, valvular degeneration caused by calcification, rheumatic
 XX heart disease, endocarditis, or complications of artificial valves;
 XX atrial fibrillation, long-QT syndrome, congestive heart failure, sinus
 XX node dysfunction, angina, heart failure, hypertension, atrial flutter,
 XX atrial fibrillation, pericardial disease, including but not limited to
 XX pericardial effusion and pericarditis, cardiomyopathies (e.g. dilated
 XX cardiomyopathy or idiopathic cardiomyopathy), myocardial infarction,
 XX coronary artery disease, coronary artery spasm, ischaemic disease,
 XX arrhythmia, sudden cardiac death, and cardiovascular developmental
 XX disorders. The invention is also useful in gene therapy. The present
 XX sequence is human napsin A protein. This sequence is used to illustrate
 XX the method of the invention

Sequence 420 AA;
 Query Match 99.7%; Score 2232; DB 6; Length 420;
 Best Local Similarity 99.8%; Pred. No. 2.6e-202;
 Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSPPPPLQPLLLPLLNVEPSGATLIRPLHRVQPGRTILRLRGWRPAPLPLKLGAPS 60
 Db 1 MSPPPPLQPLLLPLLNVEPSGATLIRPLHRVQPGRTILRLRGWRPAPLPLKLGAPS 60
 QY 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120
 Db 61 PGDKPIFVPLSNRYDVQYFGEIGLGTTPQNFTVAFTDGTSSNLWVPSRRCHFFSVPCWLHH 120
 QY 121 REDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAP 180
 Db 121 REDPKASSFQANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWPSLVFAP 180
 QY 181 AHFDGILGLGFPILSVGEVRPMDVLVEQGLLDKPVFSFVLNDRDPEDGGELVLGSDP 240
 Db 181 AHFDGILGLGFPILSVGEVRPMDVLVEQGLLDKPVFSFVLNDRDPEDGGELVLGSDP 240

Db 181 AHFDGILGLGFPILSVGVRPMDVLVEQGLLDKPFVSYFLNRDPPEPDGSELVLGGSDP 240
 Qy 241 AHYPPLTFVPTVPAYWQHMERVKVPGGLTLCAKGAAILDTGTSITGPTTEIRALH 300
 Db 241 AHYPPLTFVPTVPAYWQHMERVKVPGGLTLCAKGAAILDTGTSITGPTTEIRALH 300
 Qy 301 AAIGGIPLLAGEYIILCSEIIPKLPVAVSFLGGLGVWVFNLTADHDYVITQTRNGVRLCLSGFQA 360
 Db 301 AAIGGIPLLAGEYIILCSEIIPKLPVAVSFLGGLGVWVFNLTADHDYVITQTRNGVRLCLSGFQA 360
 Qy 361 LDVPPPPAGPWILGDVFLGTGVAVFDRGDMKSSARVGLARARTGADLGMGETAQAPPG 420
 Db 361 LDVPPPPAGPWILGDVFLGTGVAVFDRGDMKSSARVGLARARTGADLGMGETAQAPPG 420

RESULT 6

AAO20497
 ID AAO20497 standard; protein; 433 AA.
 XX AC AAO20497;

XX 27-JUN-2002 (first entry)

XX Protein of NAPI from aspartyl protease-related family.

XX Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
 KW amyloid precursor protein; tissue-specific expression control; human APP;
 KW APP pathway modulator; gene therapy.

XX Homo sapiens.

XX WO200226820-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-EP011345.

XX 29-SEP-2000; 2000US-0236893P.

XX 14-JUN-2001; 2001US-0298309P.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Cohen D, Dengler UV, Finelli AL, Freuler F, Konsolaki M;

XX Reinhardt WHEM, Zusman S;

XX WPI; 2002-315796/35.

XX N-PSDB; AAK99391.

XX New transgenic fly, containing DNA encoding an Abeta portion of human
 PT APP, useful for identifying agents which modulate the APP pathway and
 PT which can be used to treat Alzheimer's disease.

XX Example 4; Page 87-88; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA
 CC encoding a polypeptide having the Abeta portion of human amyloid
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 CC the specification. The DNA sequence is operably linked to a tissue-
 CC specific expression control sequence. Expression of the sequence gives
 CC the fly an altered phenotype. The purpose of the invention is for
 CC identifying agents that inhibit or promote the expression and/or function
 CC of genes or encoded polypeptides which modify the APP pathway. The agent
 CC is a compound, triple helix DNA, antisense oligonucleotide, double
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 CC to treat conditions such as Alzheimer's disease. The agent can be used as
 CC an APP pathway modulator or in gene therapy. This sequence represents the
 CC protein of the APP related NAPI from the aspartyl protease-related family

XX Sequence 433 AA;

Query Match 99.7%; Score 2232; DB 5; Length 433;

Best Local Similarity 99.8%; Pred. No. 2.7e-202;
 Matches: 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MSPPPLLQPLLLLLPLLNVPESGATLIRIPHRVQPGRTINLLRGHREPAELPKLGAPS 60
 Db 14 MSPPPLLQPLLLLLPLLNVPESGATLIRIPHRVQPGRTINLLRGHREPAELPKLGAPS 73
 Qy 61 PGDKPIFVPLSNTRDVQYFGEIGLGTTPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
 Db 74 PGDKPIFVPLSNTRDVQYFGEIGLGTTPQNTFVAFDTGSSNLWVPSRRCHFFSVPCWLHH 133
 Qy 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTITGGKASVIFGEALWEPSSLVPAF 180
 Db 134 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTITGGKASVIFGEALWEPSSLVPAF 193
 Qy 181 AHFDGILGLGFPILSVGVRPMDVLVEQGLLDKPFVSYFLNRDPPEPDGSELVLGGSDP 240
 Db 194 AHFDGILGLGFPILSVGVRPMDVLVEQGLLDKPFVSYFLNRDPPEPDGSELVLGGSDP 253
 Qy 241 AHYPPLTFVPTVPAYWQHMERVKVPGGLTLCAKGAAILDTGTSITGPTTEIRALH 300
 Db 254 AHYPPLTFVPTVPAYWQHMERVKVPGGLTLCAKGAAILDTGTSITGPTTEIRALH 313
 Qy 301 AAIGGIPLLAGEYIILCSEIIPKLPVAVSFLGGLGVWVFNLTADHDYVITQTRNGVRLCLSGFQA 360
 Db 314 AAIGGIPLLAGEYIILCSEIIPKLPVAVSFLGGLGVWVFNLTADHDYVITQTRNGVRLCLSGFQA 373
 Qy 361 LDVPPPPAGPWILGDVFLGTGVAVFDRGDMKSSARVGLARARTGADLGMGETAQAPPG 420
 Db 374 LDVPPPPAGPWILGDVFLGTGVAVFDRGDMKSSARVGLARARTGADLGMGETAQAPPG 433

RESULT 7

AAW37958
 ID AAW37958 standard; protein; 395 AA.
 XX AC AAW37958;

XX 21-AUG-1998 (first entry)

XX Amino acid sequence of human cathepsin polypeptide-2.

XX Human cathepsin polypeptide-2; HCP-2; metastasis; antibody; agonist;
 KW antagonists; tumour; arthritis; Alzheimer's disease; HCP-1;
 KW Huntington's disease; mucopolidosis.

XX Homo sapiens.

XX WO9813484-A1.

XX 02-APR-1998.

XX 25-SEP-1997; 97WO-US017175.

XX 26-SEP-1996; 96US-00723938.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Coleman R;

XX WPI; 1998-230698/20.

XX N-PSDB; AAV31665.

XX Human cathepsins and related nucleic acids, vectors and products - useful
 PT for treatment and diagnosis of e.g. tumours, metastases, inflammation,
 PT neurological disease etc.

XX Claim 15; Fig 5A-5D; 69pp; English.

XX This is the amino acid sequence of the human cathepsin polypeptide-2 (HCP
 CC -2), which is involved in inflammation, metastasis and peptide/proenzyme
 CC processing. HCP related products (e.g. antibodies, agonists, and
 CC antagonists) are potentially useful for treating tumours, arthritis,


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XX OS Homo sapiens.
XX PN WO9822597-A2.
XX PD 28-MAY-1998.
XX PF 20-NOV-1997; 97WO-US021684.
XX PR 20-NOV-1996; 96US-0031196P.
XX FR 09-MAY-1997; 97US-0046128P.
XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PI Keolsch G, Lin X, Tang JUN;
XX XX
XX WPI; 1998-312482/27.
XX DR N-PSDB; AAV27036.
XX XX
XX PT New isolated aspartic protease, napsin, from human liver - potentially
XX PT useful for, e.g. diagnosis and treatment of disease.
XX PS Claim 3; Fig 1; 24pp; English.
XX CC
XX CC The present sequence represents the human napsin A protein. The cDNA
XX CC sequence that produces this protein was obtained by splicing together
XX CC isolated napsin cDNA clones, which had been found by screening a human
XX CC liver cDNA library. Napsin A is an aspartic protease which was isolated
XX CC from human liver, however it has also been found to be present in other
XX CC human tissues
XX SQ Sequence 451 AA;

Query Match 84.8%; Score 1897; DB 2; Length 451;
Best Local Similarity 86.0%; Pred. No. 1.4e-170;
Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

QY 1 MSPPPPLLOPLLLPLLVNPSGATLIRIPHRVQPGRTNLLRGWREPAPLPLKLGAPS 60
DB 1 MSPPPPLLOPLLLPLLVNPSGATLIRIPHRVQPGRTNLLRGWREPAPLPLKLGAPS 60
QY 61 PGDKPIFVPLSNRYDVQFGEIGLGTTPQNFVAFDTGSSNLWVPSRCHFFSVPCWLHH 120
DB 61 PGDKPASVPLSKFLDAQFGEIGLGTTPQNFVAFDTGSSNLWVPSRCHFFSVPCWFHH 120
QY 121 RFDPKASSFQANGKFAIQGTGRVDGILSDKLTIGIKGASVIFGEALWEPSELVFAF 180
DB 121 RFNPNASSFPSPGTFKFAIQGTGRVDGILSDKLTIGIKGASVIFGEALWESSLVFTV 180
QY 181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKVFVSYLNRPDEPDGGLVILGSDP 240
DB 181 SRPDGILGLGFPILSVEGVRPPDLVLVEQGLLDKVPFSFYFNRPDEPADGGLVILGSDP 240
QY 241 AHYIPPLFVPTVPAYQIHMERYKVGSPGLTCLAKGCAALDTSITGTEIRALH 300
DB 241 AHYIPPLFVPTVPAYQIHMERYKVGSRRLTCAQGCALDITGTPVIVGTTEIRALH 300
QY 301 AAGIGPILAGBYIILCSEIPKLPVAVSLIGGVWENLTADHYIQTTRNGVRLCLSGFOA 360
DB 301 AAGIGPILAGBYIIRCSSEIPKLPVAVSLIGGVWENLTADHYIQTTRNGVRLCLSGFRA 360
QY 361 LDVPPPPAGPFWLLGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGTAAQPPG 420
DB 361 LDIASPPVPVWLLGDVFLGAYTVTVFDRGDMKSGARVGLARARPRGADLGRETAAQYRG 420

RESULT 10
ID AAY44810
XX AAY44810 standard; protein; 433 AA.
XX AC AAY44810;
XX XX
XX DT 18-MAY-2000 (first entry)

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XX DE Human Aspartic Protease-2 (NHAP-2).
XX KW Human; aspartic protease-2; NHAP-2; chromosome 19q13.3; antiallergic;
KW immunosuppressive; cytostatic; antidiabetic; antineoplastic; cancer;
KW antihypertensive; antithyroid; antibacterial; neuroprotective;
KW antidiabetic; anti-HIV; osteopathic; antihypertensive; treatment; cretinism;
KW endocrinological; hypogonadism; Sheehan syndrome; diabetes insipidus;
KW hypothyroidism; adenocarcinoma; leukaemia; immunological; amyloidosis;
KW acquired immune deficiency syndrome; AIDS; Addison's disease; arthritis;
KW osteoporosis; atherosclerosis; infection; respiratory; allergy; asthma;
KW emphysema; gene therapy; diagnosis.
XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT 1. .21
XX FT /label= "Signal_peptide"
XX FT /note= "Potential"
XX FT Protein
XX FT 22. .433
XX FT /label= "Mature NHAP-2"
XX FT /note= "Homologous to mouse aspartic protease-like
XX FT protein (GI 1906810)"
XX FT 60
XX FT Modified-site
XX FT /note= "Potential casein kinase phosphorylation site"
XX FT Modified-site
XX FT /note= "Potential Tyrosine kinase phosphorylation site"
XX FT Modified-site
XX FT /note= "Potential N-glycosylation site"
XX FT Active-site
XX FT /note= "Potential active site Asp residue characteristic
XX FT of aspartic proteases"
XX FT Modified-site
XX FT /note= "Potential protein kinase C phosphorylation site"
XX FT Modified-site
XX FT /note= "Potential N-glycosylation site"
XX FT Modified-site
XX FT /note= "Potential protein kinase C phosphorylation site"
XX FT Modified-site
XX FT /note= "Potential protein kinase C phosphorylation site"
XX FT Active-site
XX FT /note= "Potential active site Asp residue characteristic
XX FT of aspartic proteases"
XX FT Modified-site
XX FT /note= "Potential N-glycosylation site"
XX FT Modified-site
XX FT /note= "Potential casein kinase phosphorylation site"
XX FT Modified-site
XX FT /note= "Potential casein kinase phosphorylation site"
XX FT Binding-site
XX FT /note= "Potential cell attachment site"
XX FT Modified-site
XX FT /note= "Potential cAMP-cGMP-dependent protein kinase
XX FT phosphorylation site"
XX PN WO200004137-A1.
XX XX
XX PD 27-JAN-2000.
XX XX
XX PF 15-JUL-1999; 99WO-US015988.
XX PR 16-JUL-1998; 98US-00116641.
XX XX (INCY-) INCYTE PHARM INC.
XX XX Xu H, Bruno SA, Eisenboss LA, Fogliano M, Cohan VL, Bandman O;
XX WPI; 2000-182413/16.
XX DR N-PSDB; AAZ50232.
XX XX
XX PT New human aspartic protease polypeptide useful for treating and detecting

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CC	panic disorder, learning disabilities, amyotrophic lateral sclerosis,	
CC	psychoses, autism, sleep disorders), immune system disorders (e.g.	
CC	Hashimoto's thyroiditis), renal and musculo-skeletal system disorders	
CC	central nervous system disorders (e.g. multiple sclerosis, ischaemic	
CC	brain injury and/or stroke), infectious diseases, diabetes mellitus,	
CC	immunological disorders (e.g. asthma, acquired immunodeficient syndrome	
CC	(AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,	
CC	sepsis, acne, psoriasis and lupus erythematosus), neural system	
CC	disorders, respiratory disorders, olfactory disorders and wound healing.	
CC	The present sequence represents an NHP of the invention	
XX		
SQ	Sequence 390 AA;	
	Query Match	76.1%; Score 1702.5; DB 4; Length 390;
	Best Local Similarity	83.3%; Pred. No. 3e-152;
	Matches 334; Conservative	7; Mismatches 15; Indels 45; Gaps 4;
QY	21	PSGATLIRPLHRVQPGRRTLNLRGWREPAELPKLGAPSPGDKPIFVPLSNRYDVQYFG 80
Db	34	PSGATLIRPLHRVQPGRRTLNLRGWREPAELPKLGAPSPGDKPIFVPLSNYKG---- 88
QY	81	EIGLTPPQNTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSFQANGTKFAIQ 140
Db	89	-----WLHHRFDPKASTP--SSQWDQFAIQ 111
QY	141	YGTGRVDGILSEDKLTIGGIKASVIFGE--ALWPESLVPAFAHFDGILGLGFPILSVEGV 199
Db	112	YGTGRVHGILSEDKLTIGGIKASVIFGELSGTQPL--RFPFDGILGLGFPILSVEGV 169
QY	200	RPPMDVLVEQGLDKPVSFYLNRPDEPDGGBLVLGSDPAHYIPLTVPVTPPAYWQ 259
Db	170	RPPMDVLVEQGLDKPVSFYLNRPDEPDGGBLVLGSDPAHYIPLTVPVTPPAYWQ 229
QY	260	IHMVRKVGSLTCAKGCAAILDGTSLTGTETTRALHAALGIPILLAGEYIILCSE 319
Db	230	IHMVRKVGSLTCAKGCAAILDGTSLTGTETTRALHAALGIPILLAGEYIILCSE 289
QY	320	IPKLPVPSFLLGGVFNLTADHYVQITRNGVRLCLSGFQALDVPPPPAGPFWILGDVFLG 379
Db	290	IPKLPVPSFLLGGVFNLTADHYVQITRNGVRLCLSGFQALDVPPPPAGPFWILGDVFLG 349
QY	380	TYVAVFDGRGDKMSARVGLARTRGADLWGETAQAQFPFG 420
Db	350	TYVAVFDGRGEMKSARVGLARTRGADLWGETAQAQFPFG 390
	RESULT 12	
AAW57043		
AC	AAW57043 standard; protein; 449 AA.	
AC		
XX		
XX	29-JUL-1998 (first entry)	
DT		
DE	Human aspartic protease encoding cDNA SEQ ID NO:15.	
XX		
XX	Human; aspartic protease; EST; endothelin; serum amyloid A protein;	
KW	pro-Opimelanocortin prohormone.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	Misc-difference 1	/note= "encoded by NAA"
FT	Misc-difference 2	/note= "encoded by ANA"
FT	Misc-difference 410	/note= "encoded by TGA"
FT	Misc-difference 417	/note= "encoded by TGA"
FT	Misc-difference 427	/note= "encoded by TGN"
FT	Misc-difference 427	/note= "encoded by TGN"
FT	Misc-difference 433	

FT	Misc-difference 440	/note= "encoded by GMC"
FT	Misc-difference 442	/note= "encoded by TGA"
FT	Misc-difference 442	/note= "encoded by NGA"
XX	WO9811236-A1.	
PD	19-MAR-1998.	
XX		
PF	09-SEP-1997; 97WO-GB002426.	
XX		
PR	11-SEP-1996; 96GB-00018966.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM PLC.	
PA	(UYWA-) UNIV WALES.	
XX		
PI	Powell D, Kay J, Hill J;	
XX		
DR	WPI; 1998-207396/18.	
DR	N-PSDB; AAV28624.	
XX		
PT	Human aspartic protease and related DNA - which may be involved in	
PT	processing of endothelin and pro-opimelanocortin pro-hormone(s).	
XX		
PS	Claim 14; Page 23; 32pp; English.	
XX		
CC	The present sequence represents a human aspartic protease. The present	
CC	invention describes novel human aspartic proteases and also ESTs from	
CC	human cDNA libraries having partial DNA sequences which encodes an	
CC	aspartic protease. Compounds which inhibit aspartic protease, especially	
CC	antibodies can be used in therapy where needed. The protease can also be	
CC	used in therapy where needed. Important functions of aspartic proteases	
CC	are the processing of endothelin and pro-opimelanocortin prohormones.	
CC	They may also be involved in the processing of serum amyloid A protein	
XX		
SQ	Sequence 449 AA;	
	Query Match	75.0%; Score 1678.5; DB 2; Length 449;
	Best Local Similarity	81.1%; Pred. No. 6.8e-150;
	Matches 327; Conservative	18; Mismatches 55; Indels 3; Gaps 3;
QY	9	PLLLLLPLLNVEPSGATLIRPLHRVQPGRRTLNLRGWREPAELPKLGAPSPGDKPIFV 68
Db	28	PSLLLLPLLNVEPAGATLIRPLRQVHGPGRRTNLRGKPAELPKLGAPSPGDKPASV 87
QY	69	PLSNRYDVQYGEIGLTPPQNTVAFTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASS 128
Db	88	PLSKFLDAQYFGEIGLTPPQNTVAFTGSSNLWVPSRRCHFFSVPCWFHHRFNPASS 147
QY	129	SFOANGTKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWPESLVPAFAHFDGILG 188
Db	148	SFKPSGTFKFAIQYGTGRVDGILSEDKLTIGGIKASVIFGEALWESSLVFTVSRPDGILG 207
QY	189	LGPPILSVEGVRPPMDVLVEQGLDKPVSFYLNRPDEPDGGBLVLGSDPAHYIPLT 248
Db	208	LGFPILSVEGVRPPDLVLVEQGLDKPVSFYFNRPDEPVNNGSELVLGGSDPAHYIPLN 267
QY	249	FVPVTVPAYWQIHMVRKVGSLTCAKGCAAILDGTSLTGTETTRALHAALGIP 307
Db	268	FVPVTVPAYWQIHMVRKVGSLTCAKGCNAILDGTGLVLTGTETTRALHAALGIP 327
QY	308	LLAGEYIILCSEIPKLPVPSFLLGGVFNLTADHYVQITRNG--VRLCLSGFQALDVPPP 366
Db	328	LLAGEYIIRCSEIPKLPVPSLILGGVFNLTADHYVQITTRKGVRLCLSGFRALDIARA 387
QY	367	AGPFWILGDVPLGYVAVFDGRGDKMSARVGLARTRGADLWG 409
Db	388	EGPFWILGEVFWG--ICDRFDRGTXAANPSXLAGVALRGXPXSG 429
	RESULT 13	
	AAV79177	

PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226686P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228024P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231143P.
 PR 08-SEP-2000; 2000US-0231144P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 23-SEP-2000; 2000US-0234597P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

WP-; 2001-465566/50.

N-PSDB; AAS40936.

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Claim 11; SEQ ID NO 1062; 1180bp; English.

The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. influenza). The polynucleotides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 288 AA;

Query Match 60.0%; Score 1343; DB 4; Length 288;

Best Local Similarity 99.6%; Pred. No. 2.1e-118;

Matches 251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPPPLQLPLLLPLLVNVEPSGATLRPLHRVQGRITLLRWRPAPLPLKLGAPS 60

|||||

Db 3 MSPPPLLQPLLLPLLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS 62
QY 61 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRCHFFSVPCWLHH 120
Db 63 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRCHFFSVPCWLHH 122
QY 121 RFDPKASSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPVSLVFAF 180
Db 123 RFDPKASSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPVSLVFAF 182
QY 181 AHFDGILGLGFPILSVESGVRPMDVLVEQGLLDKPVFSFYLNRPDPDGGELVLGGSDP 240
Db 183 AHFDGILGLGFPILSVESGVRPMDVLVEQGLLDKPVFSFYLNRPDPDGGELVLGGSDP 242
QY 241 AHYIPPLTFVTV 252
Db 243 AHYIPPLTFVTV 254

RESULT 15
AAB85539
ID AAB85539 standard; protein; 262 AA.
XX AAB85539;
DT 25-SEP-2001 (first entry)
XX Human secreted protein (clone Id HCRM12).
DE Secreted protein; immunosuppressive; antiairthritis; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neotropic; neuroprotective; antibacterial; virucide; fungicide; human;
KW opthalmological; gene therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 231
FT /note= "Xaa can be any amino acid"
XX WO200155430-A1.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001431.
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 12-SEP-2000; 2000US-0231968P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
PI Fiscella M, Ni J, Ruben SM, Barash SC;
XX WPI; 2001-476220/51.
XX N-ESDB; AAH46949.

17 isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition.
Claim 11; Page 455-456; 482pp; English.
The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or

CC treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein
SQ Sequence 262 AA;
Query Match 59.3%; Score 1328; DB 4; Length 262;
Best Local Similarity 97.6%; Pred. No. 4.8e-117;
Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 MSPPPLLQPLLLPLLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS 60
Db 1 MSPPPLLQPLLLPLLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS 60
QY 61 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRCHFFSVPCWLHH 120
Db 61 PGDKPIFVPLSNYRDVQYFGEIGLGTTPQNTFAFDTGSSNLWVPSRCHFFSVPCWLHH 120
QY 121 RFDPKASSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPVSLVFAF 180
Db 121 RFDPKASSFOANGTKFAIQYGTGRVDGILSEDKLTIGGKASVIFGEALWEPVSLVFAF 180
QY 181 AHFDGILGLGFPILSVESGVRPMDVLVEQGLLDKPVFSFYLNRPDPDGGELVLGGSDP 240
Db 181 AHFDGILGLGFPILSVESGVRPMDVLVEQGLLDKPVFSFYLNRPDPDGGELVLGGSDP 240
QY 241 AHYIPPLTFVTV 255
Db 241 AHYIPPSFFVTVRSP 255

Search completed: June 2, 2004, 20:19:01
Job time : 103.065 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:07:29 ; Search time 14.9222 Seconds
(without alignments)
1966.411 Million cell updates/sec

Title: US-09-700-770-7

Perfect score: 459

Sequence: 1 MKLVTIFLLVITSLGYSAT.....LGPEASEAVKLLLEALSHLV 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_ivirus:*

16: sp_bacteriap:*

17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123.5	26.9	94	11 Q8CJC6	Q8CJC6 mus musculus
2	78.5	17.1	2109	8 Q32836	Q32836 pelargonium
3	76.5	16.7	1490	13 Q98TV5	Q98TV5 salmo salar
4	76.5	16.7	1519	13 Q9W750	Q9W750 salmo salar
5	75.5	16.4	1503	13 Q73677	Q73677 fundulus he
6	73.5	16.0	481	5 Q7YZ54	Q7YZ54 cryptospori
7	73.5	16.0	1518	13 Q9IAR8	Q9IAR8 salmo salar
8	73	15.9	630	16 Q836X7	Q836X7 enterococcu
9	71.5	15.6	542	17 Q8ZNV6	Q8ZNV6 pyrobaculum
10	71	15.5	488	13 Q8Q001	Q8Q001 ictalurid p
11	70.5	15.4	1358	10 Q8W2P4	Q8W2P4 oryza sativ
12	70.5	15.4	1358	10 Q7XH05	Q7XH05 oryza sativ
13	70	15.3	106	10 Q9LVP3	Q9LVP3 arabidopsis
14	70	15.3	232	16 Q8XMB4	Q8XMB4 clostridium
15	70	15.3	603	10 Q7XRL3	Q7XRL3 oryza sativ
16	70	15.3	1502	10 Q9LYZ7	Q9LYZ7 arabidopsis

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17 69.5 15.1 425 17 Q97W07
18 69.5 15.1 451 16 Q97W00
19 69.5 15.1 506 10 Q9M143
20 69.5 15.1 563 5 Q9N3Y4
21 69.5 15.1 568 16 Q97JD4
22 69.5 15.1 951 5 Q9W388
23 69 15.0 1000 11 Q8C488
24 69 15.0 1049 2 Q31100
25 69 15.0 1049 2 Q93PU4
26 68.5 14.9 208 10 Q9LRL3
27 68.5 14.9 231 2 Q9Z4I5
28 68.5 14.9 328 10 Q49847
29 68.5 14.9 335 10 Q65675
30 68.5 14.9 356 10 Q9M069
31 68.5 14.9 464 10 Q9M051
32 68.5 14.9 673 5 Q9W137
33 68.5 14.9 906 5 Q8IIG8
34 68.5 14.9 1284 12 Q8QMS9
35 68.5 14.9 1511 13 Q9I8E2
36 68 14.8 147 9 Q80190
37 68 14.8 239 16 Q66904
38 68 14.8 693 10 Q23122
39 68 14.8 1034 16 Q8AB07
40 67.5 14.7 288 16 Q98IG5
41 67.5 14.7 297 16 Q83NK5
42 67.5 14.7 297 16 Q83MX1
43 67.5 14.7 430 16 Q8P8Y8
44 67.5 14.7 485 10 Q8LPT2
45 67.5 14.7 512 10 Q9SY85

```

ALIGNMENTS

RESULT 1

Q8CJC6 PRELIMINARY; PRT; 94 AA.

AC Q8CJC6; DT 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE UGRP2 type B.

GN SCG3A1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2326074; PubMed=12438750;

RA Nimi T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodhai A.,

RA Zimonjic D.B., Keck-Waggoner C.L., Popescu N.C., Kimura S.;

RT "Cloning, expression, and chromosomal localization of the mouse gene

RT (Scg3a1, alias Ugrp2) that encodes a member of the novel uteroglobin-

RL Cytogenet. Genome Res. 97:120-127(2002).

DR EMBL; AF313457; AAN62328.1; --

DR MGD; MGI:1915912; Scgb3a1.

SQ SEQUENCE 94 AA; 9578 MW; 7C84B908A6365B59 CRC64;

Query Match 26.9%; Score 123.5; DB 11; Length 94;

Best Local Similarity 43.1%; Pred. No. 2.5e-05;

Matches 31; Conservative 10; Mismatches 16; Indels 15; Gaps 2;

QY 30 PVDKLP-----LPLDNLFPMDPLKLLKTLGIVSEHLVEGLRKCVELGPEA 78

DB 24 PVALAPAAEAAGAVGAVPSLPLSLA----ILRFILASMGIPLDPLIEGRKCVTELGPEA 79

QY 79 SEAVKGLLEALS 90

DB 80 VGAVKSLGLVLT 91

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RESULT 2
Q32836 ID Q32836 PRELIMINARY; PRT; 2109 AA.
AC Q32836;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF2280.
OS Pelargonium hortorum (Common geranium).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Geraniales; Geraniaceae; Pelargonium.
OX NCBI_TaxID=4031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94363755; PubMed=8082181;
RA Downie S.R., Katz-Dowrie D.S., Wolfe K.H., Calie P.J., Palmer J.D.;
RT "Structure and evolution of the largest chloroplast gene (ORF2280):
RT internal plasticity and multiple gene loss during angiosperm
RT evolution."
RL Curr. Genet. 25:367-378(1994).
DR EMBL; M83200; AAA73173.1; -.
DR PIR; T31352; T31352.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR008543; DUF825.
DR Pfam; PF05695; DUF825; 1.
DR SMART; SM00382; AAA; 2.
DR ATP-binding; Chloroplast.
KW SEQUENCE 2109 AA; 245645 MW; 948980477223DE8C CRC64;
SQ
Query Match 17.1%; Score 78.5; DB 8; Length 2109;
Best Local Similarity 24.0%; Pred. No. 31;
Matches 23; Conservative 16; Mismatches 24; Indels 33; Gaps 3;
QY 7 FLAVTSLCSYATAFELINKVPLFVDKLAFLPLDNLPLFPM----- 46
DB 564 FLFVLRSFLYKSLPLLSKLSK-FLLVSKVLPLLSKLLPFFVSCGNIPHRSE 622
QY 47 -----DPLKLLKTLGTSVHLVEGLRKCV 71
DB 623 IRIYELKGPVQPCNPLLESIGLHL-NKLKPLC 657
RESULT 3
Q98TY5 ID Q98TY5 PRELIMINARY; PRT; 1490 AA.
AC Q98TY5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator I.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX Chen J., Jacques C., Cutler C., Mercier B., Boeuf G., Ferec C.;
RT "Salmo salar cystic fibrosis transmembrane conductance regulator I.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF319595; AA07405.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
SQ
Query Match 16.7%; Score 76.5; DB 13; Length 1490;
Best Local Similarity 36.4%; Pred. No. 36;
Matches 28; Conservative 10; Mismatches 24; Indels 15; Gaps 3;

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QY 31 VDKLAPLPLDNLFPMDP--LKLLKLTG-----ISVHLVEGLRKCVNGLGPEAS- 79
DB 1395 LSKARILLDPESAFDLPITQLVRLKTKQSFNCTVILSEHRVPELLEQCSFLMIEGSS 1454
QY 80 ----EAVKKLLEALSHL 92
DB 1455 MKRYDSIQKLNWETSHL 1471

RESULT 5
O73677
ID O73677 PRELIMINARY; PRT; 1503 AA.
AC O73677;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]_TaxID=8078;
RP SEQUENCE FROM N.A.
RX MEDLINE=98191134; PubMed=9530103;
RA Singer T.D., Tucker S.J., Marshall W.S., Higgins C.F.;
RT "A divergent CFTR homologue: highly regulated salt transport in the
RT euryhaline teleost F. heteroclitus.";
RL Am. J. Physiol. 274:C715-C723(1998).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF000271; AAC41271.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR001140; ABC TM transp.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR005291; cAMP-cl-channel.
DR Pfam; PF00664; ABC membrane; 2.
DR Pfam; PF00005; ABC tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM00382; AAA; 2.
DR TIGRFAMs; TIGR00953; 3a01202; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Transmembrane; Transport.
SQ SEQUENCE 1503 AA; 169250 MW; B95766EFA205920 CRC64;

Query Match 16.4%; Score 75.5; DB 13; Length 1503;
Best Local Similarity 35.1%; Pred. No. 45;
Matches 27; Conservative 14; Mismatches 21; Indels 15; Gaps 4;

QY 31 VDKLAPLPLDNLFPMDP--LKLLKLTG-----GISV--EHLVEGLRKCVNGLGPEAS- 79
DB 1379 LSKARILLDPESVYLDLPITQLVRLKTKQSFNCTVILSEHKVPELLEQCSFLMIEKSS 1438
QY 80 ----EAVKKLLEALSHL 92
DB 1439 VKSYDSIQKLNWETSHL 1455

RESULT 6
O73Z54
ID O73Z54 PRELIMINARY; PRT; 481 AA.
AC O73Z54;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
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DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Glutamine synthetase, probable.
GN IMB.677.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]_TaxID=5807;
RP SEQUENCE FROM N.A.
RA Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M.,
RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
RT "Integrated mapping, chromosomal sequencing and sequence analysis of
RT Cryptosporidium parvum.";
RL Genome Res 0:0-0(2003).
DR EMBL; BX538353; CAD98273.1; -.
SQ SEQUENCE 481 AA; 54314 MW; D7BEAB422FA18886 CRC64;

Query Match 16.0%; Score 73.5; DB 5; Length 481;
Best Local Similarity 24.4%; Pred. No. 23;
Matches 19; Conservative 18; Mismatches 32; Indels 9; Gaps 1;

QY 23 LINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISVHLVEGLRKCVNGLGPEAS--- 79
DB 186 LASRRPLQAYCAPYVDRLSLRSEILLELEENIGVTVEKHHVATCOHEIGVHCSTLV 245
QY 80 ----EAVKKLLEALSH 91
DB 246 QSADIVESIRYLKIGIAH 263

RESULT 7
O9IAR8
ID O9IAR8 PRELIMINARY; PRT; 1518 AA.
AC O9IAR8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator II.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]_TaxID=8030;
RP SEQUENCE FROM N.A.
RX MEDLINE=21396404; PubMed=11504857;
RA Chen J.M., Cutler C., Jacques C., Boeuf G., Denamur E., Lecointre G.,
RA Mercier B., Cramb G., Ferec C.;
RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance
RT Regulator: Implications for Structure and Disease Models.";
RL Mol. Biol. Evol. 18:1771-1788(2001).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF161070; AAF37801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR001140; ABC TM transp.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR005291; cAMP-cl-channel.
DR Pfam; PF00664; ABC membrane; 2.
DR Pfam; PF00005; ABC tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM00382; AAA; 2.
DR TIGRFAMs; TIGR00953; 3a01202; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Transmembrane; Transport.
SQ SEQUENCE 1518 AA; 171136 MW; B3579B15820BA7F4 CRC64;
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Db 315 FLIVGSLVLSVANAF-----DISKLTPTKELTSLRPLALSR-----PEG 358
Qy 67 LRKCVNELGPEASEAVKKLLEAL 89
Db 359 MRVVVNALFGAIPSGIVNVLLVCL 381

RESULT 11
Q8W2P4 PRELIMINARY; PRT; 1358 AA.
AC Q8W2P4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative aldehyde oxidase.
GN OSJNAA0087H07.7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R.,
RA Rambo T., Saski C., Henry D., Oates R., Simmons J.;
RT "Rice Genomic Sequence";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -I- COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
DR EMBL; AC099733; AAL70116.1; -.
DR Gramene; Q8W2P4; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0004672; P:protein kinase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002888; 2Fe-2S bind.
DR InterPro; IPR006058; 2Fe2S fold BS.
DR InterPro; IPR008274; Aldoxan dh bind.
DR InterPro; IPR000674; Aldoxan dh hamm.
DR InterPro; IPR005107; CO deh flav C.
DR InterPro; IPR002346; dehydrog molyb.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF01315; Ald_xan_dh_C1.
DR Pfam; PF02738; Ald_xan_dh_C2; 1.
DR Pfam; PF03450; CO deh flav C; 1.
DR Pfam; PF00941; FAD binding_5; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF01799; fer2.2; 1.
DR ProDom; PD186071; 2Fe-2S bind; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
KW Iron; Iron-sulfur.
SQ SEQUENCE 1358 AA; 145453 MW; 75B3A692C75D537D CRC64;

Query Match 15.4%; Score 70.5; DB 10; Length 1358;
Best Local Similarity 27.9%; Pred. No. 1.4e+02;
Matches 24; Conservative 13; Mismatches 38; Indels 11; Gaps 3;

Qy 8 LLVTTISL---CSYSATAFLINKVPLPVDKLAFLPLDNLPLFMDPLKLLKTL-GISVVEHL 63
Db 407 LLISISIPDWCSDGTF-----ETFAAPRPFNGNAVSYNSAFLARSSLDAAAGSHL 459

Qy 64 VEGLRKCVNELGPEASEAVKKLLEAL 89
Db 460 IEDVRLAFGAFGSEHAIRASKVVEFL 485

RESULT 12
Q7XH05 PRELIMINARY; PRT; 1358 AA.
ID Q7XH05
Query Match 15.3%; Score 70; DB 10; Length 106;
Best Local Similarity 27.3%; Pred. No. 11;
Matches 21; Conservative 16; Mismatches 32; Indels 8; Gaps 2;

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AC Q7XH05;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative aldehyde oxidase.
GN OSJNAA0087H07.7.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10";
RL Chromosome 300:1566-1569 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Bue.l C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017054; AAP52052.1; -.
SQ SEQUENCE 1358 AA; 145452 MW; 75B3A692C75D537D CRC64;

Query Match 15.4%; Score 70.5; DB 10; Length 1358;
Best Local Similarity 27.9%; Pred. No. 1.4e+02;
Matches 24; Conservative 13; Mismatches 38; Indels 11; Gaps 3;

Qy 8 LLVTTISL---CSYSATAFLINKVPLPVDKLAFLPLDNLPLFMDPLKLLKTL-GISVVEHL 63
Db 407 LLISISIPDWCSDGTF-----ETFAAPRPFNGNAVSYNSAFLARSSLDAAAGSHL 459

Qy 64 VEGLRKCVNELGPEASEAVKKLLEAL 89
Db 460 IEDVRLAFGAFGSEHAIRASKVVEFL 485

RESULT 13
Q9LVP3 PRELIMINARY; PRT; 106 AA.
ID Q9LVP3
AC Q9LVP3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Genomic DNA, chromosome 3, P1 clone: MXE2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Columbia;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones";
RL DNA Res. 7:131-135 (2000).
DR EMBL; AB018121; BAB01992.1; -.
SQ SEQUENCE 106 AA; 11542 MW; 6AE232EFD4C5D0DD CRC64;

Query Match 15.3%; Score 70; DB 10; Length 106;
Best Local Similarity 27.3%; Pred. No. 11;
Matches 21; Conservative 16; Mismatches 32; Indels 8; Gaps 2;

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QY 1 MKLVITLIVLTISLCSYSATAFLINKVPLPVDKLPALPLDNLNLPFMDPL---KLL----- 52
Db 1 MKFTTLVLVLTIVLQSLPTLRATWVGPGDVTCPNMDVIVPCLPLTNSKILPTPHC 60
QY 53 LKLTIGISVEHLVGLRK 69
Db 61 CQVNFMMQHOITINIRK 77

RESULT 14

Q8XMB4 PRELIMINARY; PRT; 232 AA.
AC Q8XMB4
ID Q8XMB4
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein CPE0775.
GN CPE0775.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
CX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003198; BAB80481.1; -
DR InterPro; IPR007500; DUF542/ScdA_N.
DR InterPro; IPR005544; HHE.
DR Pfam; PF01794; HHE; 1.
DR Pfam; PF04405; ScdA_N; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 232 AA; 27555 MW; 5C3F5BE1FB9AE1 CRC64;

Query Match 15.3%; Score 70; DB 16; Length 232;
Best Local Similarity 32.0%; Pred. No. 25;
Matches 24; Conservative 9; Mismatches 38; Indels 4; Gaps 1;
QY 23 LINKVPLPVDKLPALPLDNLNLPFMDPLKLLKTIGISVEHLVGLRKCVNELGPEASEAV 82
Db 14 VVTVPVAVVKFNDMELDYCCGGNKSLELAKKGVDDKFDVDELNKEFKFKFNSQYV 73
QY 83 ----KLLLEALSHLV 93
Db 74 DWREKSEELISHIV 88

RESULT 15

Q7XR13 PRELIMINARY; PRT; 603 AA.
AC Q7XR13
ID Q7XR13
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNB0022F23.17 protein.
GN OSJNB0022F23.17.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,

RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606447; CAF02880.1; -
SQ SEQUENCE 603 AA; 66009 MW; EADFA4BED0C7E49A CRC64;

Query Match 15.3%; Score 70; DB 10; Length 603;
Best Local Similarity 27.4%; Pred. No. 66;

Matches 26; Conservative 12; Mismatches 29; Indels 28; Gaps 4;

QY 7 FLVLTISLCSYSATAFL-----INKVPLPVDKLPALPLDNLNLPFMDPLKL 51
Db 84 FLISIFLHCE----AYIGGIRMEWIPTSGWPEVALYPLPVLSLSQQMADEALPLTD---- 135
QY 52 LLKTLGISVEHLVGLRKCVNELGPEASEAVKKLL 86
Db 136 ---IIGLLVDHQVEASLK--EKVAKESDAALLL 165

Search completed: June 2, 2004, 20:21:27

Job time : 17.9222 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:05:19 ; Search time 3.6175 Seconds
(without alignments)
1338.637 Million cell updates/sec

Title: US-09-700-770-7

Perfect score: 459

Sequence: 1 MKLVTFILVITSLCSYAT.....IGPEASEAVKKLEALSHLV 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	459	100.0	93	1 UGR1_HUMAN	Q96p11 homo sapien
2	326	71.0	139	1 UGR1_MOUSE	Q920h1 mus musculu
3	162.5	35.4	104	1 UGR2_MOUSE	Q920d7 mus musculu
4	159	34.6	104	1 UGR2_HUMAN	Q96q11 homo sapien
5	75.5	16.4	90	1 LPB2_HUMAN	Q95969 homo sapien
6	72	15.7	153	1 YF09_METJA	Q58304 methanococ
7	68.5	14.9	1284	1 ATL1_COWPX	P16602 cowpox viru
8	68	14.8	144	1 RPC2_BPH1	P06153 bacteriophage
9	67.5	14.7	764	1 SYFB_HELPJ	Q92kf8 helicobacte
10	67	14.6	95	1 PSC3_RAT	Q92780 rattus norv
11	67	14.6	445	1 MURD_RICPR	Q92dc2 rickettsia
12	66.5	14.5	91	1 UTER_HUMAN	P11684 homo sapien
13	66.5	14.5	395	1 NIFS_AZOCH	P23120 azotobacter
14	66.5	14.5	713	1 YD21_METJA	Q58717 methanococ
15	65.5	14.3	207	1 FRL1_HIFMO	P35395 hyppophthalm
16	65.5	14.3	844	1 CNA4_RAT	P54748 rattus norv
17	65	14.2	90	1 LPFA_HUMAN	Q95968 homo sapien
18	65	14.2	356	1 Y102_BACHD	Q9kg33 bacillus ha
19	65	14.2	417	1 DCD4_VIBCH	Q9KX17 vibrio chol
20	64.5	14.1	437	1 SAHH_PYRAE	Q82uq7 pyrobaculum
21	64.5	14.1	765	1 METE_LISIN	Q92ax9 listeria in
22	64	13.9	699	1 YQQA_CAEEL	Q92999 caenorhabdi
23	63.5	13.8	282	1 ZDH1_HUMAN	Q8wvz1 homo sapien
24	63.5	13.8	432	1 HEM1_SYNXP	Q7u769 synechococ
25	63.5	13.8	749	1 PEX1_HUMAN	P78562 homo sapien
26	63.5	13.8	749	1 PEX1_MOUSE	P70669 mus musculu
27	63.5	13.8	764	1 SYFB_HELPJ	P56145 helicobacte
28	63	13.7	127	1 Y55B_MYCPN	P75047 mycoplasma
29	63	13.7	319	1 CAHC_SPIOL	P94016 spinacia ol
30	63	13.7	498	1 NDDD_ALCXX	P94212 alcaligenes
31	63	13.7	620	1 CHS5_SCHPO	Q92357 schizosacch
32	63	13.7	773	1 PAC2_PSES3	P15558 pseudomonas
33	62.5	13.6	610	1 LEPA_BUCAI	P57348 buchnera ap

34	62.5	13.6	844	1 CNA4_MOUSE	O89084 mus musculu
35	62.5	13.6	886	1 CNA4_HUMAN	P27815 homo sapien
36	62	13.5	98	1 SZ10_HUMAN	P02778 homo sapien
37	62	13.5	239	1 RF35_BACAA	P26763 bacillus an
38	62	13.5	277	1 RS2_CHLPN	Q927X9 chlamydia p
39	62	13.5	342	1 Y755_METJA	Q58165 methanococ
40	62	13.5	363	1 LEU3_PICJA	O89791 pichia jadi
41	62	13.5	529	1 IMDH_MYCLE	Q49729 mycobacteri
42	62	13.5	2210	1 RRP0_LYCVA	P14240 lymphocytic
43	61.5	13.4	454	1 APY_SOLTU	P80595 solanum tub
44	61.5	13.4	562	1 Y55L_SYNY3	P74126 synechocyst
45	61.5	13.4	2434	1 ABC2_MOUSE	P41234 mus musculu

ALIGNMENTS

RESULT 1
UGR1_HUMAN STANDARD; PRT; 93 AA.
AC Q96p11;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).
DE member 2).
GN SCGB3A2 OR UGRP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539178; PubMed=11682631;
RA Nilmi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., RA Kimura S.;
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";
RL Mol. Endocrinol. 15:2021-2036(2001).
[2]
SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., Morley K.C., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahsey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Skalska D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung.
CC -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
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CC -----
DR EMBL; AF313456; AAL26216.1; --
DR MGD; MGI:1915912; Scgb3a1.
KW Cytokine; Signal.
FT SIGNAL 21 POTENTIAL.
FT CHAIN 22 104 UTEROGLOBIN-RELATED PROTEIN 2.
SQ SEQUENCE 104 AA; 10591 MW; D62F0E601FB57A6D CRC64;

Query Match 35.4%; Score 162.5; DB 1; Length 104;
Best Local Similarity 40.0%; Pred. No. 1.1e-09;
Matches 42; Conservative 17; Mismatches 27; Indels 19; Gaps 3;

QY 1 MKLVTFILVITSLCSYSATAFLINKVPL-----PVDKLAFL-----LPDNLDPF 45

Db 1 MKLTTTFLVLCVALLSDSGVAFPMDSIAKPAVEFVAALAPAAEAVAGAVPSLPLSLA-- 58

QY 46 MDPLKLLLTGLTISVEHLVEGLKVCNVELGPEASEAVKLLLEALS 90

Db 59 --ILRFILASMGIPLDPLIEGSRKCVTELGPFAVGAVKSLGLVLT 101

RESULT 4

UGR2_HUMAN
ID UGR2_HUMAN STANDARD; PRT; 104 AA.
AC Q96QL1; Q96QL0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1).
GN SCGB3A1 OR UGRP2 OR HIN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396515; PubMed=11481438;
RA Krop I.B., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P., Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z., Belinea D., Razumovic J., Polyak K.;
RA "HIN-1, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=21531978; PubMed=11682631;
RA Niimi T., Keck-Weggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";
RL Mol. Endocrinol. 15:2021-2036(2001).
CC -!- FUNCTION: Potential growth inhibitory cytokine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in breast cancer cell lines.
CC -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.

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DR EMBL; AY040564; AAK82942.1; --
DR EMBL; AF313458; AAL26217.1; --
DR Genew; HGNC:18384; SCGB3A1.
DR MIM; 606500; --

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005125; F:cytokine activity; NAS.
DR GO; GO:0030308; P:negative regulation of cell growth; NAS.
DR GO; GO:0042127; P:regulation of cell proliferation; NAS.
KW Cytokine; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 104 UTEROGLOBIN-RELATED PROTEIN 2.
SQ CONFLICT 19 R -> A (IN REF. 2).
SQ SEQUENCE 104 AA; 10185 MW; 1083873C8FAE8015 CRC64;

Query Match 34.6%; Score 159; DB 1; Length 104;
Best Local Similarity 43.6%; Pred. No. 2.4e-09;
Matches 44; Conservative 9; Mismatches 38; Indels 10; Gaps 2;

QY 1 MKLVTFILVITSLCSYSATAFLINKVPLPVDKLAFL-----PLDNLDPMDPLKL 51

Db 1 MKLAALLGLCVALLSCS-SARAEVLGSAKPAQVPAALSAEAAAGAGTLANFLGTINPLKL 59

QY 52 LLKTTGISVEHLVEGLKVCNVELGPEASEAVKLLLEALS 92

Db 60 LLSSLGIPVNHLEGSQKCVAEELGPQAVGAVKALKALGAL 100

RESULT 5

LPFB_HUMAN
ID LPFB_HUMAN STANDARD; PRT; 90 AA.
AC Q95969;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lipophilin B precursor (Secretoglobin family 1D member 2).
GN SCGB1D2 OR LPFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99167354; PubMed=10066439;
RA Zhao C., Nguyen T., Yusifov T., Glasgow B.J., Lehrer R.I.;
RT "Lipophilins: human peptides homologous to rat prostatein.";
RL Biochem. Biophys. Res. Commun. 256:147-155(1999).
CC -!- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND ESTRAMUSTINE, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER. MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION WAS FOUND IN SKELETAL MUSCLE. EXPRESSED AS WELL IN THYMUS, TRACHEA, KIDNEY, STEROID RESPONSIVE TISSUES (PROSTATE, TESTIS, UTERUS, BREAST AND OVARY), AND SALIVARY GLAND.
CC -!- SIMILARITY: Belongs to the uteroglobin family. Lipophilin subfamily.

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DR EMBL; AJ224172; CAAL1864.1; --
DR Genew; HGNC:18396; SCGB1D2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000329; Uteroglobin subf.

DR InterPro; IPR006038; Uteroglobin subf.

DR Pfam; PF01099; Uteroglobin; 1.

DR PRINTS; PR00486; UTEROGLOBIN.

KW Signal.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 90 LIPOPHILIN B.

SQ SEQUENCE 90 AA; 9925 MW; 17BB555ED035DIAF CRC64;

Query Match 16.4%; Score 75.5; DB 1; Length 90;

```
Best Local Similarity 27.0%; Pred. No. 0.57;
Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

QY 1 MKLVITFLVTSICSYSAFALINKVPLVVDKVLAPLDNLIIPFM---DPL-KLLIKTL 56
Db 1 KLLSVCLLVTLALCCYQANA-----BFCPALVSELDLDFPISBFLFKLSLAKF 49
QY 57 GISVEHLVE--GLRKCYNELGPE-----ASEAVKKLEALS 90
Db 50 DAPPEAVALKGVKARCTDQMSLQKRSIAEVLVVKILKKS 89

RESULT 6
ID YF09 METJA STANDARD; PRT; 153 AA.
AC Q58904;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein M31509.
GN M31509.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96377993; PubMed=8689087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Smith M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Hurt H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL jannaschii."
CC Science 273:1058-1073 (1996).

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-----
DR EMBL; U67592; AAB99534.1; -.
DR PIR; D64488; D64488.
DR TIGR; M31509; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 17718 MW; 081ABEDC831685B CRC64;

Query Match 15.7%; Score 72; DB 1; Length 153;
Best Local Similarity 28.8%; Pred. No. 2.2;
Matches 19; Conservative 17; Mismatches 22; Indels 8; Gaps 2;

QY 22 FLINKVPLVDKVLAPLDNLIIPFMDPLKLLIKTLGTSVEHLVGLRKCYNELGPEASEA 81
Db 93 YVMKKIP-----GDLPLDDIV--VDNPLITGTIFIVGVRIKALHEDIERIKHEIE 144
QY 82 VKKLE 87
Db 145 AKKVL 150

Query Match 15.7%; Score 72; DB 1; Length 153;
Best Local Similarity 28.8%; Pred. No. 2.2;
Matches 19; Conservative 17; Mismatches 22; Indels 8; Gaps 2;

QY 22 FLINKVPLVDKVLAPLDNLIIPFMDPLKLLIKTLGTSVEHLVGLRKCYNELGPEASEA 81
Db 93 YVMKKIP-----GDLPLDDIV--VDNPLITGTIFIVGVRIKALHEDIERIKHEIE 144
QY 82 VKKLE 87
Db 145 AKKVL 150

RESULT 7
ATI COMXPX
ID ATI COMXPX STANDARD; PRT; 1284 AA.
AC P16602;
DT 01-AUG-1990 (Rel. 15, Created)
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DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE A-type inclusion protein (ATI).
GN ATI.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CPRO6;
RX MEDLINE=88089536; PubMed=2826668;
RA Funahashi S., Sato T., Shida H.;
RT "Cloning and characterization of the gene encoding the major protein
RL of the A-type inclusion body of cowpox virus."
RL J. Gen. Virol. 69:35-47 (1988).
RN [2]
RP SEQUENCE OF 1-109 FROM N.A.
RX MEDLINE=88111568; PubMed=2828037;
RA Patel D.D., Pickup D.J.;
RT "Messenger RNAs of a strongly-expressed late gene of cowpox virus
RL contain 5'-terminal poly(A) sequences."
RL EMBO J. 6:3787-3794 (1987).
CC -!- FUNCTION: NATURE VIRUSES ARE OCCLUDED INTO THE ATI, AND IT HAS
CC BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING
CC DISSEMINATION FROM ANIMAL TO ANIMAL.
CC -!- MISCELLANEOUS: A CHARACTERISTIC FEATURE OF ATI IS THE FORMATION OF
CC LARGE MASSES WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF
CC INFECTED CELLS.
-----
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-----
DR EMBL; D00319; BAA00222.1; -.
DR PIR; X06343; CAA29650.1; -.
DR PIR; JQ0006; WMVZAI.
DR InterPro; IPR007596; Pox_A_type_inc.
DR Pfam; PF04508; Pox_A_type_inc; 14.
KW Late protein; Repeat.
FT DOMAIN 611 912 10 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 611 637 1.
FT REPEAT 638 665 2.
FT REPEAT 666 689 3.
FT REPEAT 690 720 4.
FT REPEAT 721 751 5.
FT REPEAT 752 780 6.
FT REPEAT 781 811 7.
FT REPEAT 812 842 8.
FT REPEAT 843 871 9.
FT REPEAT 872 912 10.
SQ SEQUENCE 1284 AA; 150329 MW; F7904C9E1DE8D012 CRC64;

Query Match 14.9%; Score 68.5; DB 1; Length 1284;
Best Local Similarity 36.0%; Pred. No. 45;
Matches 27; Conservative 7; Mismatches 24; Indels 17; Gaps 5;

QY 30 PVDKVLAPLDNLIIPFMDPLKLLIKTLGTSVEHLVGLRKCYNELG--- 75
Db 364 PVKVVQSKPDDGITPNPFDPDYVTTTKVLGIADYQLVINKLIEWLDCBEECNGG 423
QY 76 ---PEASEAVKKLE 87
Db 424 EYKTELEAKRKLTE 438

RESULT 8
RPC_BPPH1
ID RPC_BPPH1 STANDARD; PRT; 144 AA.
```

P06153; P15239;
 01-JAN-1988 (Rel. 06, Created)
 01-APR-1990 (Rel. 14, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Immunity repressor phi-105.
 OS Bacteriophage phi-105.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 CC Lambda-like viruses.
 CC NCBI_TaxID=10717;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA MEDLINE=86283656; PubMed=3135184;
 RA van Kaer L., Gansemans Y., van Montagu M., Dhaese P.;
 RT "Interaction of the Bacillus subtilis phage phi 105 repressor DNA: a
 RT genetic analysis";
 RL EMBO J. 7:859-866(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85297750; PubMed=2993999;
 RA Dhaese P., Seurinck J., de Smet B., van Montagu M.;
 RT "Nucleotide sequence and mutational analysis of an immunity repressor
 RT gene from Bacillus subtilis temperate phage phi 105";
 RL Nucleic Acids Res. 13:5441-5455(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86056972; PubMed=3934047;
 RA Cully D.F., Garro A.J.;
 RT "Nucleotide sequence of the immunity region of Bacillus subtilis
 RT bacteriophage phi 105: identification of the repressor gene and its
 RT mRNA and protein products";
 RL Gene 38:153-164(1985).
 CC -!- SIMILARITY: Contains 1 HTH cro/C1-type DNA-binding domain.
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 CC
 CC EMBL; X02799; CAA26567.1; ALT INIT.
 CC EMBL; M11920; AAA88396.1; -.
 DR PIR; A91579; RPBPF5.
 DR InterPro; IPR001387; HTH_3.
 DR Pfam; PF01381; HTH_3; 1.
 DR SMART; SM00530; HTH_XRE; 1.
 DR PROSITE; PS0943; HTH_CROCl; 1.
 KW Transcription regulation; Repressor; DNA-binding; Early protein.
 FT DOMAIN 7 61 HTH CRO/C1-TYPE.
 FT DNA_BIND 18 37 H-T-H MOTIF (POTENTIAL).
 SQ SEQUENCE 144 AA; 16520 MW; EEED6EB3E4B34A1E CRC64;
 Query Match 14.8%; Score 68; DB 1; Length 144;
 Best Local Similarity 24.3%; Pred. No. 5.3;
 Matches 25; Conservative 13; Mismatches 33; Indels 32; Gaps 2;
 QY 23 LINKVPLVDKLAFLDNLFPMDPLKLLKTLGIVSEHLV-----64
 DB 21 LAEKANLSRYLADIERDYNPSLSLEAVAGALGQVSAIVGEETLIKEQAEYNSKEE 80
 QY 65 -----EGLRKVKNELG-----PEASEAVKKLLEALSHLV 93
 DB 81 KOIAKMEERKDKSLDGLSFSGEPMSQAEVSLMEAMHIV 123
 RESULT 9
 ID SYF8 HELPJ STANDARD; PRT; 764 AA.
 AC Q9ZKF8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)
 DE (Phenylalanine--tRNA ligase beta chain) (PheRS).
 GN PHE" OR JHP0979.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 CC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 CC Helicobacteraceae; Helicobacter.
 CC NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Lind L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori";
 RL Nature 397:176-180(1999).
 CC -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
 CC diphosphate + L-phenylalanyl-tRNA(Phe).
 CC -!- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain
 CC family. Subfamily 1.
 CC -!- SIMILARITY: Contains 1 tRNA-binding domain.
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 CC
 CC EMBL; AE001527; AAD06558.1; -.
 DR PIR; F71863; F71863.
 DR HAMAP; MF 00283; -; 1.
 DR InterPro; IPR005146; B3_4.
 DR InterPro; IPR005147; B5.
 DR InterPro; IPR005121; Fdx-AntiCB.
 DR InterPro; IPR008994; Nucleic_acid_O8.
 DR InterPro; IPR004532; PheT_bact.
 DR InterPro; IPR002547; tRNA_bind.
 DR Pfam; PF03483; B3_4; 1.
 DR Pfam; PF03484; B5; 1.
 DR Pfam; PF03147; Fdx-ACB; 1.
 DR Pfam; PF01588; tRNA_bind; 1.
 DR TIGRFAMs; TIGR00472; PheT_bact; 1.
 DR PROSITE; PS50886; TRBD; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; Magnesium; RNA-binding; tRNA-binding;
 KW Complete proteome.
 FT DOMAIN 38 148 TRNA-BINDING.
 FT METAL 433 433 MAGNESIUM (BY SIMILARITY).
 FT METAL 439 439 MAGNESIUM (VIA CARBONYL OXYGEN)
 FT METAL 439 439 (BY SIMILARITY).
 FT METAL 442 442 MAGNESIUM (BY SIMILARITY).
 FT METAL 443 443 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 764 AA; 85154 MW; 70BDADF202FED425 CRC64;
 Query Match 14.7%; Score 67.5; DB 1; Length 764;
 Best Local Similarity 38.0%; Pred. No. 33;
 Matches 27; Conservative 10; Mismatches 27; Indels 7; Gaps 4;
 QY 20 TAPLINVPLPVDKLAFLDNLFPMDPLKLLKTLGIVSEHLVVEGLVKCVNELGPFA 78
 DB 690 TAFSKIKKAL---KDAQIPNLSEILP-LDIFKESGNTIALSRVCVTHSLKTLND--EEV 743
 QY 79 SEAVKKLLEAL 89
 DB 744 NSAVQKALEIL 754

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CC EMEL; V01263; CAA24577.1; -.
DR EMEL; W71245; AAA41965.1; -.
DR FIR; A92395; BORT3.
DR InterPro; IPR003627; Mambg/prostatn.
DR InterPro; IPR00329; Uteroglobln_subf.
DR InterPro; IPR006038; Uteroglobln_subf.
DR Pfam; PF01099; Uteroglobln; 1.
DR ProDom; PD029354; Mambg/prostatn; 1.
DR ProSITE; PS00403; UTEROGLOBIN_1; FALSE_NEG.
DR ProSITE; PS00404; UTEROGLOBIN_2; 1.
KW SIGNAL; Glycoprotein; Steroid-binding.
FT CHAIN 1 18 PROSTATIC STEROID-BINDING PROTEIN C3
FT CHAIN 19 95 CHAIN.
FT CAEBOHYD 35 35 N-LINKED (GLCNAC. .).
FT CONFLICT 53 53 D -> A (IN REF. 3).
FT CONFLICT 79 79 G -> S (IN REF. 2).
FT CONFLICT 95 95 F7F7F1A0C882E375 CRC64;
SQ SEQUENCE 95 AA; 10730 MW; 7F7F7F1A0C882E375 CRC64;
Query Match 14.6%; Score 67; DB 1; Length 95;
Best Local Similarity 27.5%; Pred. No. 4.4;
Matches 25; Conservative 21; Mismatches 37; Indels 8; Gaps 3;
-----
QY 1 MKLVITFLVLTISLCYSY-SATAFLINKVPLVDVKLAPLPLDNLPLPMDPLKLLKTL-GI 58
Db 1 MKLVFLVLTIPICCVASGSGCI-----LDEVIRGTINSTVTLHDYMKLVKPYVDH 54
QY 59 SVEHLVEGLRKCVNELGPSEAVKLLLEAL 89
Db 55 FTEKAVKQKQCFDQDQTKLENVGVNMEAI 85
-----
RESULT 11
MURD_RICPR
ID MURD_RICPR STANDARD; PRT; 445 AA.
AC Q92DC2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (UDP-N-
DE acetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid
DE adding enzyme).
DN MURD OR RP410.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsia; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RX Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RX Sichevitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RX Eriksson A.-S., Winkler H.H., Kurland C.G.;
RA "The genome sequence of Rickettsia prowazekii and the origin of
RA mitochondria."
RT Nature 396:133-140(1998).
RL Nature 396:133-140(1998).
CC -!- FUNCTION: Cell wall formation. Catalyzes the addition of
CC glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-
CC alanine (UMA) (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanine +
CC glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-
CC glutamate.
CC -!- PATHWAY: Peptidoglycan biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the murCDEF family.
-----
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PSC3_RAT
ID PSC3_RAT STANDARD; PRT; 95 AA.
AC P02780; Q63463;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Prostatic steroid-binding protein C3 chain precursor (Prostatein
DE peptide C3).
DE Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83082848; PubMed=6294095;
RA Parker M.G., White R., Hurst H., Needham M., Tilly R.;
RT "Prostatic steroid-binding protein. Isolation and characterization of
RT C3 genes."
RL J. Biol. Chem. 258:12-15(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83238526; PubMed=6190812;
RA Viskochil D.H., Perry S.T., Lea O.A., Stafford D.W., Wilson E.M.,
RA French F.S.;
RT "Isolation of two genomic sequences encoding the Mr = 14,000 subunit
RT of rat prostatein."
RL J. Biol. Chem. 258:8861-8866(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92165796; PubMed=1537831;
RA Tan J.A., Marschke K.B., Ho K.-C., Perry S.T., Wilson E.M.,
RA French F.S.;
RT "Response elements of the androgen-regulated C3 gene."
RL J. Biol. Chem. 267:4456-4466(1992).
RN [4]
RP ERRATUM.
RX MEDLINE=92218467; PubMed=1339454;
RA Tan J.A., Marschke K.B., Ho K.C., Perry S.T., Wilson E.M.,
RA French F.S.;
RL J. Biol. Chem. 267:7958-7958(1992).
RN [5]
RP SEQUENCE OF 19-95.
RX MEDLINE=91189769; PubMed=7014218;
RA Pecers B., Rombauts W., Mous J., Heyns W.;
RT "Structural studies on rat prostatic binding protein. The primary
RT structure of its glycosylated component C3."
RL Eur. J. Biochem. 115:115-121(1981).
CC -!- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY
CC GLYCOPROTEIN OF VENTRAL PROSTATE GLAND. STEROID-BINDING PROTEIN;
CC CAN BIND NON-POLAR STEROIDS, CHOLESTEROL AND A GROUP OF SMALL
CC PROLINE-RICH PEPTIDES.
CC -!- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED
CC C1, C2 AND C3. THESE FORM COVALENT C1:C3 (F) AND C2:C3 (S)
CC HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC
CC (C1:C3/C3:C2) PROSTATEIN MOLECULES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: VENTRAL PROSTATE.
CC -!- INDUCTION: ANDROGEN DEPENDENT, AS SHOWN BY THE DECREASE IN THE
CC LEVEL OF THE PROTEIN FOLLOWING CASTRATION.
CC -!- MISCELLANEOUS: C3 IS ENCODED BY TWO DIFFERENT GENES.
CC -!- SIMILARITY: Belongs to the uteroglobln family. Lipophilin
CC subfamily.
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CC -----
DR EMBL; AJ235271; CAA14867.1; -;
DR PIR; A71699; A71699.
DR HSSP; P14900; 1UAG.
DR HAMAP; MF 00639; -; 1.
DR InterPro; IPR000713; Mur_ligase.
DR InterPro; IPR004101; Mur_ligase_C.
DR InterPro; IPR005762; MurD.
DR Pfam; PF01225; Mur_ligase; 1.
DR Pfam; PF02875; Mur_ligase_C; 1.
DR TIGRFAMs; TIGR01087; murD; 1.
KW Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
KW ATP-binding; Complete proteome.
FT NP_BIND 111 117 ATP (POTENTIAL).
SQ SEQUENCE 445 AA; 50129 MW; B9CCCF7437FB7AA6 CRC64;

Query Match 14.6%; Score 67; DB 1; Length 445;
Best Local Similarity 32.0%; Pred. No. 22;
Matches 31; Conservative 12; Mismatches 24; Indels 30; Gaps 6;

QY 6 IFLLV-----TISCSYSATAFLINKVPLPVDKLAFLPLDNLIPFMDPLKLLKTLGISVE 61
DB 221 IFVLLKQDSIKLIPSVTKILKNGISIVDDKIH-----DNDLYKFLN---KNL----- 268
QY 62 HLVEGLKCKNELGPSEAV-----KKLLEALS 90
DB 269 ---QGLHCNEN---IAASAVAKIIGLESKKILESIS 299

RESULT 12

UTER_HUMAN STANDARD; PRT; 91 AA.
AC F11684; Q9UCM2; Q9UCM4;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Clara cell phospholipid-binding protein precursor (CCPBP) (Clara cells
DE 10 kDa secretory protein) (CC10) (Uteroglobin) (Urine protein 1)
DE (UPI).
DE SCGB1A1 OR UGB OR CC10 OR CCSP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=89000784; PubMed=3167058;
RA Singh G., Katyal S.L., Brown W.E., Phillips S., Kennedy A.L.,
RA Anthony J., Squeglia N.;
RT "Amino-acid and cDNA nucleotide sequences of human Clara cell 10 kDa
RT protein.";
RL Biochim. Biophys. Acta 950:329-337(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95250987; PubMed=7733299;
RA Hay J.G., Danel C., Chu C., Crystal R.G.;
RT "Human CC10 gene expression in airway epithelium and subchromosomal
RT locus suggest linkage to airway disease.";
RL Am. J. Physiol. 268:L565-L575(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=92388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-18 FROM N.A.
RX MEDLINE=93250776; PubMed=1284526;
RA Wolf M., Klug J., Hackenberg R., Gessler M., Grzeschik K.-H.,
RA Beato M., Suske G.;
RT "Human CC10, the homologue of rabbit uteroglobin: genomic cloning,
RT chromosomal localization and expression in endometrial cell lines.";
RL Hum. Mol. Genet. 1:371-378(1992).
RN [5]
RP SEQUENCE OF 22-74.
RC TISSUE=Urine;
RX MEDLINE=93016476; PubMed=1400743;
RA Okutani R., Itoh Y., Hirata H., Kasahara T., Mukaida N., Kawai T.;
RT "Simple and high-yield purification of urine protein 1 using
RT immunoaffinity chromatography: evidence for the identity of urine
RT protein 1 and human Clara cell 10-kilodalton protein.";
RL J. Chromatogr. A 577:25-35(1992).
RN [6]
RP SEQUENCE OF 22-45.
RC TISSUE=Urine;
RX MEDLINE=93009001; PubMed=1395029;
RA Bernard A., Roels H., Lauwerys R., Witters R., Gielens C.,
RA Soumillon A., Van Damme J., De Ley M.;
RT "Human urinary protein 1: evidence for identity with the Clara cell
RT protein and occurrence in respiratory tract and urogenital
RT secretions.";
RL Clin. Chim. Acta 207:239-249(1992).
RN [7]
RP SEQUENCE OF 22-33.
RX MEDLINE=21648993; PubMed=11788998;
RA Chafouri B., Stahlbom B., Tagesson C., Lindahl M.;
RT "Newly identified proteins in human nasal lavage fluid from
RT non-smokers and smokers using two-dimensional gel electrophoresis and
RT peptide mass fingerprinting.";
RL Proteomics 2:112-120(2002).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95393197; PubMed=7664082;
RA Um and T.C., Swaminathan S., Singh G., Warty V., Furey W.,
RA Pletcher J., Sax M.;
RT "Structure of a human Clara cell phospholipid-binding protein-ligand
RT complex at 1.9-A resolution.";
RL Nat. Struct. Biol. 1:538-545(1994).
CC -1- FUNCTION: BINDS PHOSPHATIDYLCHOLINE, PHOSPHATIDYLINOSITOL,
CC POLYCHLORINATED BIPHENYLS (PCB) AND WEAKLY PROGESTERONE, POTENT
CC INHIBITOR OF PHOSPHOLIPASE A2.
CC -1- SUBUNIT: Homodimer; antiparallel disulfide-linked.
CC -1- TISSUE SPECIFICITY: Clara cells (nonciliated cells of the
CC surface epithelium of the pulmonary airways).
CC -1- SIMILARITY: Belongs to the uteroglobin family.
CC -----
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DR EMBL; X13197; CAA31584.1; -
DR EMBL; U01101; AAA81885.1; -
DR EMBL; U01102; AAA18297.1; -
DR EMBL; BC004481; AAA04481.1; -
DR EMBL; X59875; CAA42532.1; -
DR PIR; JS0036; JS0036.
DR PIR; S26651; S26651.
DR HSSP; P02779; IUTG.
DR GENE; HGNC:12523; SCGB1A1.
DR GO; GO:007566; P:embryo implantation; TAS.
DR InterPro; IPR006039; Uterogl.
DR InterPro; IPR003628; Uteroglobn subf.
DR InterPro; IPR000329; Uteroglobln subf.
DR InterPro; IPR006038; Uteroglobln subf.
DR Pfam; PF01099; Uteroglobln; 1.
DR PRINTS; PR00486; UTEROGLOBIN.
DR ProDom; PD012475; Uteroglobn_sub; 1.
DR SMART; SM00096; UTG; 1.
DR PROSITE; PS00403; UTEROGLOBIN_1; 1.
DR PROSITE; PS00404; UTEROGLOBIN_2; 1.
DR Phospholipase A2 inhibitor; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 91
FT DISULFID 24 24
FT DISULFID 90 90
FT VARIANT 56 56
FT VARIANT 68 68
FT CONFLICT 24 24
FT SEQUENCE 91 AA; 9994 MW; FE65ACA678F12ABD CRC64;
Query Match 14.5%; Score 66.5; DB 1; Length 91;
Best Local Similarity 25.2%; Pred. No. 4.7;
Matches 26; Conservative 16; Mismatches 30; Indels 31; Gaps 3;
QY 1 MKLAVTFLVLTISCSYATFLINKVLPVDPKLPDLNLPFMDPLKLLKLTGISV 60
DB 1 MKLAVTFLVLTALCCSSASA-----EICP-----SFQVETLLMDTSSY 42
QY 61 EHLVE-----GLRKCYNELGPEASEAVKKLEALS 90
DB 43 EAMELFSPQDMREAGAKLKLVDTLTPQKPRESIIMKMEKIA 85
RESULT 13
NIFS AZOCH STANDARD; PRT; 395 AA.
AC P23120;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Cysteine desulfurase (EC 4.4.1.-) (Nitrogenase metalloclusters biosynthesis protein nifs).
GN NIFS.
OS Azotobacter chroococcum mcd 1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91358323; PubMed=1885524;
RA Evans D.J., Jones R., Woodley P.R., Wilborn J.R., Robeson R.L.;
RT "Nucleotide sequence and genetic analysis of the Azotobacter chroococcum nifUSVWZM gene cluster, including a new gene (nifp) which encodes a serine acetyltransferase."
RL J. Bacteriol. 173:5457-5469(1991).
CC -!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY SIMILARITY).
CC
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CC -!- COPACTOR: Pyridoxal phosphate (By similarity).
CC -!- SURUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent aminotransferases. Nifs/iscs subfamily.
CC
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CC
CC EMBL; M60090; AAA22160.1; -
CC PIR; B43706; B43706.
CC InterPro; IPR000192; Aminotrans_V.
CC Pfam; PF00866; aminotran_5; 1. CLASS 5; 1.
CC PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
CC Nitrogen fixation; Lyase; Pyridoxal phosphate.
FT INIT MET 0 BY SIMILARITY.
FT BINDING 198 198 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT ACT_SITE 318 318 BY SIMILARITY.
FT SEQUENCE 395 AA; 43165 MW; 909F70995B312BDA CRC64;
Query Match 14.5%; Score 66.5; DB 1; Length 395;
Best Local Similarity 28.9%; Pred. No. 21;
Matches 24; Conservative 18; Mismatches 30; Indels 11; Gaps 4;
QY 12 ISLCSYSAT-AFLINKVPLVDKLPDLNLPFMDPLKLLKLTGISVE---HLVSG 66
DB 100 LSLCDYLASEGYTVHK--LPVDKKGRLDLDHVASLINDVAVSVWANNETGLTFPVEE 157
QY 67 LRKCYNELG-----PEASEAVKKL 85
DB 158 MAEMADEGIMFETDAVQVRKL 180
RESULT 14
YD21 METJA STANDARD; PRT; 713 AA.
ID YD21 METJA
AC Q58717;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical protein MJ1321.
GN MJ1321.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RC MEDLINE=9637999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hrust M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91358323; PubMed=1885524;
RA Evans D.J., Jones R., Woodley P.R., Wilborn J.R., Robeson R.L.;
RT "Nucleotide sequence and genetic analysis of the Azotobacter chroococcum nifUSVWZM gene cluster, including a new gene (nifp) which encodes a serine acetyltransferase."
RL J. Bacteriol. 173:5457-5469(1991).
CC -!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY SIMILARITY).
CC
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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	78.5	17.1	2109	2	T31352	hypothetical prote	
2	72	15.7	153	2	D64488	hypothetical prote	
3	70	15.3	1502	2	T49309	hypothetical prote	
4	69.5	15.1	425	2	H90415	hypothetical prote	
5	69.5	15.1	451	2	A96920	probable ABC trans	
6	69.5	15.1	506	2	F85016	probable RING zinc	
7	69.5	15.1	568	2	E97066	membrane associate	
8	68.5	14.9	335	2	T05268	hypothetical prote	
9	68.5	14.9	356	2	D85406	hypothetical prote	
10	68.5	14.9	464	2	T47710	glucuronosyl trans	
11	68.5	14.9	1284	1	WMVZAI	A-type inclusion p	
12	68	14.8	147	1	RPBP5	immunity repressor	
13	68	14.8	239	2	D70359	conserved hypothet	
14	68	14.8	693	2	C86364	hypothetical prote	
15	67.5	14.7	512	2	A86238	protein F14N23.31	
16	67.5	14.7	566	2	AD0816	nitrate/nitrite sen	
17	67.5	14.7	764	2	F71863	phenylalanine-TRNA	
18	67	14.6	95	1	B0RT3	prostatic steroid-	
19	67	14.6	445	2	A71699	UDP-n-acetylmuramo	
20	66.5	14.5	91	2	JS00336	Clara cell 10K pro	
21	66.5	14.5	128	2	T15017	hypothetical prote	
22	66.5	14.5	396	2	B43706	nitrogenase cofact	
23	66.5	14.5	713	2	H64464	hypothetical prote	
24	66	14.4	379	2	F96565	hypothetical prote	
25	66	14.4	415	2	G75179	hypothetical prote	
26	66	14.4	793	2	C83260	hypothetical prote	
27	66	14.4	983	2	H72510	probable ribonucle	
28	66	14.4	2471	2	T42977	large tegument pro	
29	65.5	14.3	192	2	F72559	hypothetical prote	

membrane associated chemotaxis sensory transducer protein (MSP domain and HAMP domain)
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: E97066
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97066
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-568 <KUR>
A:Cross-references: GB:AS001437; PIDN:AAK79320.1; PID:gl5024285; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1352

Query Match 15.1%; Score 69.5; DB 2; Length 568;
Best Local Similarity 24.8%; Pred. No. 27;
Matches 27; Conservative 19; Mismatches 44; Indels 19; Gaps 3;

QY 1 MKLVIFLLVITSLGYSATAPLFLINKVPLVDKL---APLPDNLPLFMDPLKLLKLTIG 57
DB 186 MGILIIILISILSFAVATILNNIVNIKKLVYATSIANNLALADIHINSSDELG 245

QY 58 I---SVEHLVEGLKVCNELGPEAS-----EAVKLLLEALS 90
DB 246 VLAESFNKVRMLRSLINKINTESSNVTDAAYNLQNTQSSKALEQIA 294

RESULT 8
T05268
Hypothetical protein T4L20.60 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
C:Accession: T05268
R:Bevan, M.; Terry, N.; Ardiles, W.; Buyssehaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, September 1998
A:Reference number: Z15406
A:Accession: T05268
A:Molecule type: DNA
A:Residues: 1-335 <BEV>
A:Cross-references: EMBL:AL023094
A:Experimental source: cultivar Columbia; BAC clone T4L20
C:Genetics:
A:Map position: 4
A:Note: intron positions not resolved
A:Note: T4L20.60
C:Superfamily: beta-1,3-glucanase

Query Match 14.9%; Score 68.5; DB 2; Length 335;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 20; Conservative 10; Mismatches 17; Indels 3; Gaps 2;

QY 41 NILPFMDPLKLLKLTIGISVEHLVEGLKVCNELGPEASFAVKLLLEALS 90
DB 80 NVLPFFYPASKIMLTITVGNEI--LMSNDPNLVNQLLP-AMQNVQKALEAVS 126

RESULT 9
D85406
Hypothetical protein AT4g34480 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: D85406
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85406
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-356 <STO>
A:Cross-references: GB:NC_001268; NID:g7270398; PIDN:CAB80165.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g34480
A:Map position: 4
C:Superfamily: beta-1,3-glucanase

Query Match 14.9%; Score 68.5; DB 2; Length 356;
Best Local Similarity 40.0%; Pred. No. 21;
Matches 20; Conservative 10; Mismatches 17; Indels 3; Gaps 2;

QY 41 NILPFMDPLKLLKLTIGISVEHLVEGLKVCNELGPEASFAVKLLLEALS 90
DB 101 NVLPFFYPASKIMLTITVGNEI--LMSNDPNLVNQLLP-AMQNVQKALEAVS 147

RESULT 10
T47710
Glucuronosyl transferase-like protein - Arabidopsis thaliana
N:Alternate names: protein F1116.120
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
C:Accession: T47710
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24473
A:Accession: T47710
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <BEN>
A:Cross-references: EMBL:AL161667
A:Experimental source: cultivar Columbia; BAC clone F1116
C:Genetics:
A:Map position: 3
A:Introns: 162/1
A:Note: F1116.120
C:Superfamily: flavonol O3-glucosyltransferase

Query Match 14.9%; Score 68.5; DB 2; Length 464;
Best Local Similarity 30.6%; Pred. No. 28;
Matches 22; Conservative 15; Mismatches 28; Indels 7; Gaps 3;

QY 13 SLCSYSATAPLFLINKVPLVDKLAPLPDNLPLFMDPLKLLKLTIGISVEHLVEGLKVCN 72
DB 142 TFCAYTAPFLIDKGYLPQGSR---LDELVTLEPLK--VKDLPVKTKEPGLNRIIN 196

QY 73 EL--GPEASEAV 82
DB 197 DMVEGAKLSSGV 208

RESULT 11
WMVZAI
A-type inclusion protein - cowpox virus (strain CPROG)
C:Species: cowpox virus
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jun-2000
C:Accession: JQ0006; S01495
R:Funahashi, S.; Sato, T.; Shida, H.
J. Gen. Virol. 69, 35-47, 1988
A:Title: Cloning and characterization of the gene encoding the major protein of the
A:Reference number: JQ0006; MUID:88089536; PMID:2826668
A:Accession: JQ0006
A:Molecule type: DNA
A:Residues: 1-1284 <FUN>
A:Cross-references: GB:D00319; NID:g221140; PIDN:BAA00222.1; PID:g221141
R:Patel, D.D.; Pickup, D.J.
EMBO J. 6, 3787-3794, 1987
A:Title: Messenger RNAs of a strongly-expressed late gene of cowpox virus contain 5'
A:Reference number: S01494; MUID:8811568; PMID:2828037
A:Accession: S01495
A:Molecule type: DNA
A:Residues: 1-109 <PAT>

A;Cross-references: EMBL:X06343
C;Superfamily: Cowpox virus A-type inclusion protein
C;Keywords: inclusion protein

Query Match 14.8%; Score 68.5; DB 1; Length 1284;
Best Local Similarity 36.0%; Pred. No. 82;
Matches 27; Conservative 7; Mismatches 24; Indels 17; Gaps 5;
QY 30 PVDKGLAPLDNLT---PWDP--LKLLKT-LGIS-----VEHLVEGLRKCQNELG--- 75
DB 364 PVKVGSKDDGITYNPEDPDYPTITKTVLGIADYQLVINKLIEWLDKCEECGNG 423
QY 76 ---PEASEAVKKLE 87
DB 424 EYKTELEAKRKUTE 438

RESULT 12
RPBPF5
C;Species: Bacillus phage phi-105
A;Note: host Bacillus subtilis
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000
C;Accession: A93579; A91535; S02459; T13543; A24339; A24521
R;Dhaese, P.; Seuring, J.; De Smet, B.; Van Montagu, M.
Nucleic Acids Res. 13, 5441-5455, 1985
A;Title: Nucleotide sequence and mutational analysis of an immunity repressor gene from
A;Reference number: A93579; MUID:85297750; PMID:2993999
A;Accession: A93579
A;Molecule type: DNA
A;Residues: 1-147 <DHA>
A;Cross-references: GB:X02799; NID:g15455; PIDN:CAA26567.1; PID:g579178
R;Cully, D.F.; Garro, A.J.
Gene 38, 153-164, 1985

A;Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage P
A;Reference number: A91535; MUID:86056972; PMID:3934047
A;Accession: A91535
A;Molecule type: DNA
A;Residues: 1-147 <CUL>
R;van Kaer, L.; Gansseman, Y.; van Montagu, M.; Dhaese, P.
EMBO J. 7, 859-866, 1988
A;Title: Interaction of the Bacillus subtilis phage phi105 repressor with operator DNA:
A;Reference number: S02459; MUID:88283656; PMID:3135184
A;Accession: S02459
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 4-147 <VAN>
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y.
submitted to the EMBL Data Library, July 1998
A;Description: Complete nucleotide sequence of Bacillus subtilis phage phi-105.
A;Reference number: 217688
A;Accession: T13543
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 4-147 <KOB>
A;Cross-references: EMBL:AB016282; PIDN:BAA36660.1

A;Start codon: GTG
C;Superfamily: phage phi-105 immunity repressor protein
C;Keywords: DNA binding; early protein; repressor; transcription regulation

Query Match 14.8%; Score 68; DB 1; Length 147;
Best Local Similarity 24.3%; Pred. No. 9.2;
Matches 25; Conservative 13; Mismatches 33; Indels 32; Gaps 2;
QY 23 LINKVPLPVDKLAFLPDLNLTLPFMDPLKLLKTGLISVEHLV----- 64
DB 24 LAEKANLGRSYLADIERDRYNPSLTLEAVAGALGIQVSAIVGEETLIKKEQAEYNKEE 83
QY 65 -----EGLRKCQNELG-----PEASEAVKKLEALSHLV 93
DB 84 KDIAKMEIEIRKDLKSDGLSFGSPMSEQAEVSLMEAMHIV 126

RESULT 13
D70359

conserved hypothetical protein aq_674 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: D70359
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.
V.

Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70359
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-239 <AQF>
A;Cross-references: GB:AE000701; NID:g2983260; PIDN:AAC06868.1; PID:g2983274; GB:AE01
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_674

Query Match 14.8%; Score 68; DB 2; Length 239;
Best Local Similarity 32.6%; Pred. No. 15;
Matches 28; Conservative 15; Mismatches 27; Indels 16; Gaps 5;
QY 9 LVTISLC--SYSATAPLINKVLPVDKLAFLPDLNLTLPFMDPLKLLKTGLISVEHLV 66
DB 160 LVLLSPCFRLYELTEVLSN-FNLPRLKLS-----LIYPTLKRARLAITVSKN-VKG 210
QY 67 LRKC-----VNELGPEASEAVKKLE 87
DB 211 QLECDKPLIINKENGEYTBVKQLLE 236

RESULT 14
C86364

hypothetical protein F19G10.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 19-Apr-2002
C;Accession: C86364
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Ali
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-693 <STO>
A;Cross-references: GB:AE005172; NID:g2462833; PIDN:AAB72168.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
C;Superfamily: ferric reductase FRE2

Query Match 14.8%; Score 68; DB 2; Length 693;
Best Local Similarity 31.8%; Pred. No. 48;
Matches 34; Conservative 14; Mismatches 37; Indels 22; Gaps 5;

QY 6 IFLL-VTISLCSYSATAPLINK-----VPLPVDKLAFLPL----DNILPFMDPL----- 49
DB 584 IYLLAISIVVATSTVAMLCNKKSYFKGLYQNVDAISPLMIESPDQLLEFNTIHYGER 643
QY 50 ----KLLKLTGLISVEHLVEGLRKCQNELGPEAS--EAVKKLEALS 90
DB 644 PNLKLLVGLKSSVGVIVCGPRKREEVAKICSGSAANLQFESIS 690


```

; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-915-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60
DB 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

```

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RESULT 2
US-10-199-670-244
; Sequence 244, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-670-244

```

```

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60
DB 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

RESULT 3
US-10-201-858-244
; Sequence 244, Application US/10201858
; Publication No. US2004003837A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60
DB 1 MKLVTFILVTISLCSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTIGISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

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RESULT 4
US-10-205-890-244
; Sequence 244, Application US/10205890
; Publication No. US20040048334A1

Query Match	100.0%;	Score 459;	DB 12;	Length 93;
Best Local Similarity	100.0%;	Pred. No. 2.3e-44;		
Matches 93:	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy 1 MKNTIFLIVTISLSYSATAFLINKVPLPVDKLAPLDNDILPFMDPIKLLKLTGISV 60

D6 1 MKNTIFLIVTISLSYSATAFLINKVPLPVDKLAPLDNDILPFMDPIKLLKLTGISV 60

Qy

61 EHIVEGLRKCVELGPASEAVKKILEALSHLV 93
|||||

Dp

61 EHIVEGLRKCVELGPASEAVKKILEALSHLV 93
|||||

```

RESULT 5
US-102-008-024-244
; Sequence 244, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
;

```

; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Fan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels

	Qy	Qy	Db	Qy	Db
1	MKLVTFLLVTTISLCSYSATAFLINKVPLVDVKLAPLPLDNTILPMDPDKLLLTGLISV	60	1	MKLVTFLLVTTISLCSYSATAFLINKVPLVDVKLAPLPLDNTILPMDPDKLLLTGLISV	60
61	EHLVEGLRKCVMNELGPEASEAVKKLEALSHLV	93	61	EHLVEGLRKCVMNELGPEASEAVKKLEALSHLV	93

RESULT 6
US-10-2C1-853-244
; Sequence 244, Application US/10201853
; Publication No. US20040053358A1


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; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1997-10-24

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFILVTTSLCSYSATAFINKVPLPVDKLAFLPDNLTLPFMDPLKLLKTGIVS 60
Db 1 MKLVTFILVTTSLCSYSATAFINKVPLPVDKLAFLPDNLTLPFMDPLKLLKTGIVS 60

QY 61 EHLVEGLRCKVNLGPSEAVKLLLEALSHLV 93
Db 61 EHLVEGLRCKVNLGPSEAVKLLLEALSHLV 93

RESULT 7
US-10-174-581-244
; Sequence 244, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
```


Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

RESULT 9

US-10-176-749-244
; Sequence 244, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176, 749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

RESULT 10

US-10-176-914-244
; Sequence 244, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176, 914
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

RESULT 11

US-10-176-915-244
; Sequence 244, Application US/10176915
; Publication No. US20030017544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C110
; CURRENT APPLICATION NUMBER: US/10/176, 915
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-244

Query Match 100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
Db 1 MKLVTFLLVTSLSYSATAFLINKVPLPVDKLAFLPLDNLFPMDPLKLLKLTGISV 60
QY 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
Db 61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93

RESULT 12

US-10-176-484-244
; Sequence 244, Application US/10176484
; Publication No. US20030059876A9
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James

```

; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C64
; CURRENT APPLICATION NUMBER: US/10/176,484
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-176-484-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSICSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTGLISV 60
DB 1 MKLVTFLLVTSICSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTGLISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93

RESULT 13
US-10-180-550-244
; Sequence 244, Application US/10180550
; Publication No. US20030064440A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C149
; CURRENT APPLICATION NUMBER: US/10/180,550
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-180-550-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSICSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTGLISV 60
DB 1 MKLVTFLLVTSICSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTGLISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93

RESULT 14
US-10-180-550-244
; Sequence 244, Application US/10180550
; Publication No. US20030064440A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C149
; CURRENT APPLICATION NUMBER: US/10/180,550
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-180-550-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVTSICSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTGLISV 60
DB 1 MKLVTFLLVTSICSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTGLISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93

RESULT 15
US-10-187-738-244
; Sequence 244, Application US/10187738
; Publication No. US20030064442A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C241
; CURRENT APPLICATION NUMBER: US/10/187,738
; CURRENT FILING DATE: 2002-07-02
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-187-738-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-183-014-244
; Sequence 244, Application US/10183014
; Publication No. US20030064441A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C170
; CURRENT APPLICATION NUMBER: US/10/183,014
; CURRENT FILING DATE: 2002-06-26
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-183-014-244

Query Match      100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLVTFLLVTSICSYSATAFLINKVPLPVDKLAFLPDLNLPMDPLKLLKLTGLISV 60

QY 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
DB 61 EHLVEGLRKCYNELGPEASEAVKKLLEALSHLV 93
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Qy	1	MKLVTFLLVTISLCSYSATAFLINKVPLPVDKLAFLPLDNILPFMDPLKLLKTLGTSV	60
Db	1		60
Qy	61	EHLVEGLRKCYNELGPEASEAVKKLEALSHLV	93
Db	61		93

Search completed: June 2, 2004, 20:25:18
Job time : 17.5802 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 20:16:40 ; Search time 6.48136 Seconds
(without alignments)
740.773 Million cell updates/sec

Title: US-09-700-770-7
Perfect score: 459
Sequence: 1 MKLVTFLLVTSICSYSAT.....LGPEASEAVKLLLEALSHLV 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pdp.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pdp.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pdp.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pdp.*
5: /cgn2_6/ptodata/2/iaa/PTCUS.COMB.pdp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	459	100.0	93	2	US-08-964-725-14
2	84	18.3	17	2	US-08-964-725-15
3	77	16.8	15	2	US-08-964-725-18
4	77	16.8	18	2	US-08-964-725-19
5	76	16.6	17	2	US-08-964-725-17
6	75.5	16.4	90	3	US-08-821-451A-4
7	75.5	16.4	90	3	US-09-263-810-4
8	75.5	16.4	90	3	US-08-912-276-15
9	75.5	16.4	90	4	US-09-583-169-4
10	75.5	16.4	90	4	US-09-215-818-6
11	75.5	16.4	90	4	US-09-467-602A-6
12	73	15.9	446	4	US-09-134-000C-3434
13	69	15.0	95	3	US-08-821-451A-27
14	69	15.0	95	3	US-09-263-810-27
15	69	15.0	95	4	US-09-583-169-27
16	67.5	14.7	421	4	US-09-328-352-7140
17	67	14.6	95	1	US-08-455-896-7
18	67	14.6	95	2	US-08-933-149-7
19	67	14.6	95	3	US-09-082-343-7
20	67	14.6	95	3	US-09-082-253-7
21	67	14.6	95	4	US-09-162-622-7
22	67	14.6	95	4	US-09-509-015-7
23	67	14.6	95	5	PCT-US96-08235-7
24	66.5	14.5	91	1	US-08-455-896-8
25	66.5	14.5	91	2	US-08-933-149-8
26	66.5	14.5	91	2	US-09-082-343-8
27	66.5	14.5	91	3	US-09-082-253-8

Sequence 1, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 5830, Ap
Sequence 28767, A
Sequence 4739, Ap
Sequence 16, Appl
Sequence 6, Appli
Sequence 6372, Ap
Sequence 9300, Ap
Sequence 22, Appl
Sequence 22, Appl
Sequence 3880, Ap
Sequence 21, Appl
Sequence 7, Appli
Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-964-725-14
; Sequence 14, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian C.
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: No. 5939265e
US-08-964-725-14

Query Match 100.0%; Score 459; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLVTFILVITISLSYSATAFINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGTSV 60
Db 1 MKLVTFILVITISLSYSATAFINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGTSV 60

Qy 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93
Db 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93

RESULT 2
US-08-964-725-15
; Sequence 15, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLAS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5939265e
; US-08-964-725-18

Query Match 16.8%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 LRKCVNELGPEASEA 81
Db 1 LRKCVNELGPEASEA 15

RESULT 4
US-08-954-725-19
; Sequence 19, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice

MOLECULE TYPE: No. 5939265e
US-08-964-725-14

Query Match 100.0%; Score 459; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLVTFILVITISLSYSATAFINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGTSV 60
Db 1 MKLVTFILVITISLSYSATAFINKVPLVDKLAFLPLDNLTPMDPLKLLKLTGTSV 60

Qy 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93
Db 61 EHLVEGLRKCVELGPEASEAVKLEALSHLV 93

RESULT 2
US-08-964-725-15
; Sequence 15, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLAS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5939265e
; US-08-964-725-15

Query Match 18.3%; Score 84; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; APPLICANT: FRIEDMAN, Paula N.
;; APPLICANT: GORDON, Julian C.
;; APPLICANT: HODGES, Steven C.
;; APPLICANT: KLASS, Michael R.
;; APPLICANT: KRATOCHVIL, Jon D.
;; APPLICANT: ROBERTS-RAPP, Lisa
;; APPLICANT: RUSSELL, John C.
;; APPLICANT: STROUPE, Steven D.
;; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
;; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Abbott Laboratories
;; STREET: 100 Abbott Park Road
;; CITY: Abbott Park
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60064-3500
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/964,725
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Becker, Cheryl L.
;; REGISTRATION NUMBER: 35,441
;; REFERENCE/DOCKET NUMBER: 5997.US.P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 847/935-1729
;; TELEFAX: 847/938-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: No. 5939265e
;; US-08-964-725-19
Query Match 16.8%; Score 77; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 77 EASEAVKKLLEALSHLV 93
Db 1 EASEAVKKLLEALSHLV 17
RESULT 5
US-08-964-725-17
; Sequence 17, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Abbott Laboratories
;; STREET: 100 Abbott Park Road
;; CITY: Abbott Park
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60064-3500
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/964,725
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Becker, Cheryl L.
;; REGISTRATION NUMBER: 35,441
;; REFERENCE/DOCKET NUMBER: 5997.US.P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 847/935-1729
;; TELEFAX: 847/938-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: No. 5939265e
;; US-08-964-725-17
Query Match 16.6%; Score 76; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 LKLTGLISVHLEVL 67
Db 1 LKLTGLISVHLEVL 16
RESULT 6
US-08-821-451A-4
; Sequence 4, Application US/08821451A
; Patent No. 6066724
; GENERAL INFORMATION:
; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,451A
; FILING DATE: March 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,724


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; FILING DATE: March 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-821-451A-4

Query Match 16.4%; Score 75.5; DB 3; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

QY 1 MKLVTFILVITSLCSYSATAFINKVPLVDKLAFLPLDNLILPFM---DPL-KLLKTL 56
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MKLSVCLLLVTLALCCYQANA-----EFCPALVSELDFFFTISEPLFKLSLAKF 49

QY 57 GISVEHIVE--GLRKCVELGPE-----ASEAVKLLLEALS 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 50 DAPPEAAVKLGVRKCTDQMSLQKRSLLIAEVLVILKCKS 89

US-09-263-810-4
; Sequence 4, Application US/09263810
; Patent No. 6174992
; GENERAL INFORMATION:
; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,810
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/821,451
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN

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US-09-263-810-4
Query Match 16.4%; Score 75.5; DB 3; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

QY 1 MKLVTFILVITSLCSYSATAFINKVPLVDKLAFLPLDNLILPFM---DPL-KLLKTL 56
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MKLSVCLLLVTLALCCYQANA-----EFCPALVSELDFFFTISEPLFKLSLAKF 49

QY 57 GISVEHIVE--GLRKCVELGPE-----ASEAVKLLLEALS 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 50 DAPPEAAVKLGVRKCTDQMSLQKRSLLIAEVLVILKCKS 89

US-08-912-276-15
; Sequence 15, Application US/08912276
; Patent No. 6183952
; GENERAL INFORMATION:
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Stroupe, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,276
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5972.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6183952e
; US-08-912-276-15

Query Match 16.4%; Score 75.5; DB 3; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;

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Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;
QY 1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAFLPLDNLIPFM---DPL-KLLKTL 56
Db 1 MKLSVCLLLVTALCCYQANA-----EFCPALVSELDOFFFISEPLFKLSLAKF 49
QY 57 GISVEHLVE--GLRKCVELGPE-----ASEAVKLLLEALS 90
Db 50 DAPPEAVALKGVKRCCTDQMSLQKRSLSIAEVLVKILKCS 89
RESULT 9
US-09-583-169-4
; Sequence 4, Application US/09583169
; Patent No. 6338948
; GENERAL INFORMATION:
; APPLICANT: Colpitts, Tracey
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
; TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
; FILE REFERENCE: 5972 US P2
; CURRENT APPLICATION NUMBER: US/09/215,818A
; CURRENT FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/912,276
; EARLIER FILING DATE: 1997-08-17
; EARLIER APPLICATION NUMBER: 08/697,105
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: 08/912,149
; EARLIER FILING DATE: 1997-08-15
; EARLIER APPLICATION NUMBER: 08/697,106
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-215-818-6
Query Match 16.4%; Score 75.5; DB 4; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;
QY 1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAFLPLDNLIPFM---DPL-KLLKTL 56
Db 1 MKLSVCLLLVTALCCYQANA-----EFCPALVSELDOFFFISEPLFKLSLAKF 49
QY 57 GISVEHLVE--GLRKCVELGPE-----ASEAVKLLLEALS 90
Db 50 DAPPEAVALKGVKRCCTDQMSLQKRSLSIAEVLVKILKCS 89
RESULT 11
US-09-467-602A-6
; Sequence 6, Application US/09467602A
; Patent No. 6552164
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
; TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
; FILE REFERENCE: 5972 US P5
; CURRENT APPLICATION NUMBER: US/09/467,602A
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 08/215,818
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 08/912,276
; PRIOR FILING DATE: 1997-08-17
; PRIOR APPLICATION NUMBER: US 08/697,105
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: US 08/912,149
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: US 08/697,106
; PRIOR FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-467-602A-6
Query Match 16.4%; Score 75.5; DB 4; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;
QY 1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAFLPLDNLIPFM---DPL-KLLKTL 56

Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;
QY 1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAFLPLDNLIPFM---DPL-KLLKTL 56
Db 1 MKLSVCLLLVTALCCYQANA-----EFCPALVSELDOFFFISEPLFKLSLAKF 49
QY 57 GISVEHLVE--GLRKCVELGPE-----ASEAVKLLLEALS 90
Db 50 DAPPEAVALKGVKRCCTDQMSLQKRSLSIAEVLVKILKCS 89
RESULT 9
US-09-583-169-4
; Sequence 4, Application US/09583169
; Patent No. 6338948
; GENERAL INFORMATION:
; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/583,169
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/821,451
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-583-169-4
Query Match 16.4%; Score 75.5; DB 4; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;
QY 1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAFLPLDNLIPFM---DPL-KLLKTL 56
Db 1 MKLSVCLLLVTALCCYQANA-----EFCPALVSELDOFFFISEPLFKLSLAKF 49
QY 57 GISVEHLVE--GLRKCVELGPE-----ASEAVKLLLEALS 90
Db 50 DAPPEAVALKGVKRCCTDQMSLQKRSLSIAEVLVKILKCS 89
RESULT 10
US-09-215-818-6
; Sequence 6, Application US/09215818A
; Patent No. 6379671

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Matches 25; Conservative 21; Mismatches 37; Indels 8; Gaps 3;
Qy 1 MKLVTFLLVTVISCSY-SATAFLINKVPLVDKLAFLDNLIPFMDPLKLLKLTGIS 59
| | | | | : | | | | : | | | | : | | | | :
Db 1 MKLVFLLVTVIPICCVASGCSI-----LDEVIRGTINSTVTLHDYMKLVKPYVQAH 54
| | | | | : | | | | : | | | | : | | | | :
Qy 60 -VEHLVEGLRKCVNELGPEASEAVKLLLEAL 89
| | | | | : | | | | : | | | | : | | | | :
Db 55 FTEKAVKQKQCFDQTDKLTLENVGVNMEAI 85
| | | | | : | | | | : | | | | : | | | | :

RESULT 15
US-09-583-169-27
; Sequence 27, Application US/09583169
; Patent No. 6338948
; GENERAL INFORMATION:
; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,169
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/821,451
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-583-169-27

Query Match 15.0%; Score 69; DB 4; Length 95;
Best Local Similarity 27.5%; Pred.No. 0.71; 37; Indels 8; Gaps 3;
Matches 25; Conservative 21; Mismatches 37; Indels 8; Gaps 3;
Qy 1 MKLVTFLLVTVISCSY-SATAFLINKVPLVDKLAFLDNLIPFMDPLKLLKLTGIS 59
| | | | | : | | | | : | | | | : | | | | :
Db 1 MKLVFLLVTVIPICCVASGCSI-----LDEVIRGTINSTVTLHDYMKLVKPYVQAH 54
| | | | | : | | | | : | | | | : | | | | :
Qy 60 -VEHLVEGLRKCVNELGPEASEAVKLLLEAL 89
| | | | | : | | | | : | | | | : | | | | :
Db 55 FTEKAVKQKQCFDQTDKLTLENVGVNMEAI 85
| | | | | : | | | | : | | | | : | | | | :

Search completed: June 2, 2004, 20:23:15
Job time : 7.48136 secs

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OM protein - protein search, using sw model

Run on: June 2, 2004, 19:59:24 ; Search time 22.1572 Seconds
(without alignments)
1185.931 Million cell updates/sec

Title: US-09-700-770-7
Perfect score: 459
Sequence: 1 MKLVITFLVLTISLCSYAT.....LGPSEAVKLLLEALSHLV 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	459	100.0	93	AAW62068	Human lun
2	459	100.0	93	AAW62068	Human lun
3	459	100.0	93	AAW62068	Human lun
4	459	100.0	93	AAW62068	Human lun
5	459	100.0	93	AAW62068	Human lun
6	459	100.0	93	AAW62068	Human lun
7	459	100.0	93	AAW62068	Human lun
8	459	100.0	93	AAW62068	Human lun
9	459	100.0	93	AAW62068	Human lun
10	459	100.0	93	AAW62068	Human lun
11	459	100.0	93	AAW62068	Human lun
12	459	100.0	93	AAW62068	Human lun
13	459	100.0	93	AAW62068	Human lun
14	459	100.0	93	AAW62068	Human lun
15	459	100.0	93	AAW62068	Human lun
16	459	100.0	93	AAW62068	Human lun
17	459	100.0	93	AAW62068	Human lun
18	459	100.0	93	AAW62068	Human lun
19	459	100.0	93	AAW62068	Human lun
20	459	100.0	93	AAW62068	Human lun
21	459	100.0	93	AAW62068	Human lun
22	459	100.0	93	AAW62068	Human lun
23	459	100.0	93	AAW62068	Human lun
24	459	100.0	93	AAW62068	Human lun
25	459	100.0	93	AAW62068	Human lun

26	459	100.0	93	ABU89473	Human PRO
27	459	100.0	93	ABU86314	Human sec
28	459	100.0	93	ABU67527	Human sec
29	459	100.0	93	ABU80555	Human PRO
30	459	100.0	93	ABR99473	Human sec
31	459	100.0	93	ABR98863	Human sec
32	459	100.0	93	ABO16386	Human sec
33	459	100.0	93	ABR92286	Human sec
34	459	100.0	93	ABO18927	Human sec
35	459	100.0	93	ABR78348	Human sec
36	459	100.0	93	ABU85084	Novel hum
37	459	100.0	93	ABO00223	Novel hum
38	459	100.0	93	ABO11555	Human sec
39	459	100.0	93	ABO02200	Human sec
40	459	100.0	93	ABO88774	Novel hum
41	459	100.0	93	ABU83469	Human sec
42	459	100.0	93	ABO06270	Novel hum
43	459	100.0	93	ABR59306	Human sec
44	459	100.0	93	ABO09368	Human sec
45	459	100.0	93	ABO19232	Novel hum

ALIGNMENTS

RESULT 1
AAW62068
ID AAW62068 standard; protein; 93 AA.
XX
AC AAW62068;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human lung tissue gene LUI03 protein.
XX
KW Human; lung tissue gene; LUI03; detection; lung cancer; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9H20143-A1.
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US020680.
XX
PR 05-NOV-1996; 96US-00744211.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Cohen M, Friedman PN, Gordon J, Hodges SC, Klass MR;
PI Kratochwill JD, Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI: 1998-286957/25.
XX
N-PSDB; AAV38069, AAV38070.
XX
Lung tissue derived polynucleotide LUI03 - useful to detect, diagnose, stage, monitor, prognosis, prevent, treat or determine pre-disposition to lung disease, e.g. lung cancer.
XX
Claim 20; Page 70; 86pp; English.
XX
The present sequence represents the protein for lung tissue gene LUI03. A method has been developed for detecting the presence of a target LUI03 polynucleotide in a test sample, comprising: (a) contacting the sample with at least 1 LUI03-specific polynucleotide, and (b) detecting the target LUI03 polynucleotide in the test sample, where the LUI03 polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519 bp nucleic acid sequence given in AAV38066 to AAV38070. The methods and products of the present invention may be used to detect, diagnose, stage, monitor, prognosis, prevent, treat or determine the predisposition diseases and conditions of the lung, e.g. lung cancer

Sequence 93 AA;

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us-09-700-770-7.rag

Db 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93

Query Match 100.0%; Score 459; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 5.6e-47;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPMDPLKLLKLTGLISV 60
 Db 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPMDPLKLLKLTGLISV 60
 QY 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93
 Db 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93

RESULT 2
 AAY28334
 ID AAY28334 standard; protein; 93 AA.
 AC AAY28334;
 XX
 XX 19-OCT-1999 (first entry)
 XX
 XX LU103 specific amino acid consensus sequence.
 XX
 XX LU103; amino acid; lung cancer; detection; FISH;
 KW Fluorescent in situ hybridisation; protein.
 XX
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX US5939265-A.
 PN
 XX 17-AUG-1999.
 PD
 XX 05-NOV-1997; 97US-00964725.
 PF
 XX 05-NOV-1996; 96US-00744211.
 PR
 XX (ABBO) ABBOTT LAB.
 PA
 XX Friedman PN, Gordon J, Hodges SC, Cohen M, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD, Klass MR;
 FI
 XX WPI; 1999-468402/39.
 DR
 DR N-PSDB; AAX99424.

Polynucleotides useful for detecting, diagnosing and monitoring diseases of the lung such as lung cancer.
 XX Claim 20; Col 53; 36pp; English.
 PS
 XX The 507 base pair sequence of a LU103 specific polynucleotide was derived from a consensus of the isolated sequences from clones 1235095, 1235531 and 1379417. This sequence was then scanned for open reading frames. An ORF was found and this polypeptide was produced. The polynucleotides and methods are useful for detecting, diagnosing, staging, monitoring or predicting diseases and conditions of the lung, such as lung cancer. The polynucleotides may be used to produce probes for use in fluorescent in situ hybridization (FISH) technology to perform chromosomal analysis and identify cancer specific alterations such as deletions
 XX
 XX Sequence 93 AA;
 SQ
 Query Match 100.0%; Score 459; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 5.6e-47;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPMDPLKLLKLTGLISV 60
 Db 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPMDPLKLLKLTGLISV 60
 QY 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93

Query Match 100.0%; Score 459; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 5.6e-47;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPMDPLKLLKLTGLISV 60
 Db 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPMDPLKLLKLTGLISV 60
 QY 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93

Db 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93
 RESULT 3
 AAY44456
 ID AAY44456 standard; protein; 93 AA.
 AC AAY44456;
 XX
 XX 27-MAR-2000 (first entry)
 DT
 XX Human lung specific gene protein lng101.
 DE
 XX Lung Specific Gene; LSG; lng101; human; diagnostic marker; prognosticate;
 KW lung cancer; diagnosis.
 KW
 XX Homo sapiens.
 OS
 XX WO9960160-A1.
 PN
 XX 25-NOV-1999.
 PD
 XX 12-MAY-1999; 99WO-US010344.
 PF
 XX 21-MAY-1998; 98US-0086212P.
 PR
 XX (DIAD-) DIADEXUS LLC.
 PA
 XX Yang F, Macina RA, Sun Y;
 PI
 XX WPI; 2000-116320/10.
 DR
 DR N-PSDB; AAZ29721.
 XX
 XX A new method for diagnosing, monitoring and staging lung cancer.
 PT
 XX
 XX Example 2; Page 36; 40pp; English.
 PS
 XX The present sequence is a lung specific gene (LSG) protein lng101 from human clone ID 126758. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control
 CC
 XX
 XX Sequence 93 AA;
 SQ
 Query Match 100.0%; Score 459; DB 3; Length 93;
 Best Local Similarity 100.0%; Pred. No. 5.6e-47;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPMDPLKLLKLTGLISV 60
 Db 1 MKLVTFILVTISLCSYSATAFLINKVPLVDKLAFLPMDPLKLLKLTGLISV 60
 QY 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93
 Db 61 EHLVEGLRKCVCNELGPEASEAVKLLLEALSHLV 93
 RESULT 4
 AAY87289
 ID AAY87289 standard; protein; 93 AA.
 AC AAY87289;
 XX
 XX 11-MAY-2000 (first entry)
 DT
 XX Human signal peptide containing protein HSP66 SEQ ID NO:66.
 DE
 XX Human; signal peptide-containing protein; HSP66; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neotropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

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PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.

PS Claim 11; Fig 244; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders

XX Sequence 93 AA;

Query Match 100.0%; Score 459; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.6e-47;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLVTFLLVLTISLCSYSAFLINKVPLVDKLAFLPLDNIIPFMDPLKLLKTLGIVS 60
Db 1 MKLVTFLLVLTISLCSYSAFLINKVPLVDKLAFLPLDNIIPFMDPLKLLKTLGIVS 60

QY 61 EHLVEGLRKCVELGPEASEAVKLLLEASHLV 93
Db 61 EHLVEGLRKCVELGPEASEAVKLLLEASHLV 93

RESULT 6

ABU58521
ID ABU58521 standard; protein; 93 AA.

AC ABU58521;

XX 15-APR-2003 (first entry)

XX Human PRO polypeptide #122.

XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.

XX Homo sapiens.

XX US2003027272-A1.

XX 06-FEB-2003.

XX 21-JUN-2002; 2002US-00176492.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 17-OCT-1997; 97US-0062250P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0063120P.

XX 24-OCT-1997; 97US-0063121P.

XX 28-OCT-1997; 97US-0063540P.

XX 28-OCT-1997; 97US-0063541P.

XX 28-OCT-1997; 97US-0063544P.

XX 28-OCT-1997; 97US-0063564P.

PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078866P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 15-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 05-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.

PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	02-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100389P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	25-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-00168978.
Query Match	100.0%;	Score 459; DB 6; Length 93;
Best Local Similarity	100.0%;	Pred. No. 5.6e-47;
Matches	93; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Cy	1 MKLVTFILVTISLCSYSATAFLNKKVPLVDKGLAPLDNLPMDPKLLIKTLGISV	60
Dd	1 MKLVTFILVTISLCSYSATAFLNKKVPLVDKGLAPLDNLPMDPKLLIKTLGISV	60
Cy	61 EHLVEGLRCKVNLGPEASEAVKKLEALSHIV	93
Dd	61 EHLVEGLRCKVNLGPEASEAVKKLEALSHIV	93
RESULT 7		
ABU88069		
ID		

PR	23-SEP-1998;	98US-0101477P.	PR	18-DEC-1997;	97US-0068017P.
PR	24-SEP-1998;	98US-0101738P.	PR	10-MAR-1998;	98US-0077450P.
PR	24-SEP-1998;	98US-0101739P.	PR	11-MAR-1998;	98US-0077632P.
PR	24-SEP-1998;	98US-0101743P.	PR	11-MAR-1998;	98US-0077649P.
PR	24-SEP-1998;	98US-0101922P.	PR	20-MAR-1998;	98US-0078866P.
PR	25-SEP-1998;	98US-0101786P.	PR	20-MAR-1998;	98US-0078939P.
PR	25-SEP-1998;	98US-0102207P.	PR	27-MAR-1998;	98US-0079664P.
PR	25-SEP-1998;	98US-0102240P.	PR	27-MAR-1998;	98US-0079786P.
PR	25-SEP-1998;	98US-0102330P.	PR	31-MAR-1998;	98US-0080107P.
PR	29-SEP-1998;	98US-0102331P.	PR	31-MAR-1998;	98US-0080194P.
PR	30-SEP-1998;	98US-0102487P.	PR	01-APR-1998;	98US-0080327P.
PR	30-SEP-1998;	98US-0102570P.	PR	01-APR-1998;	98US-0080333P.
PR	30-SEP-1998;	98US-0102571P.	PR	08-APR-1998;	98US-0081049P.
PR	01-OCT-1998;	98US-0102684P.	PR	08-APR-1998;	98US-0081070P.
PR	01-OCT-1998;	98US-0102687P.	PR	09-APR-1998;	98US-0081195P.
PR	02-OCT-1998;	98US-0102965P.	PR	15-APR-1998;	98US-0081838P.
PR	06-OCT-1998;	98US-0103258P.	PR	15-APR-1998;	98US-0082568P.
Query Match 100.0%; Score 459; DB 6; Length 93;			PR	21-APR-1998;	98US-0082569P.
Best Local Similarity 100.0%; Pred. No. 5.6e-47;			PR	22-APR-1998;	98US-0082704P.
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			PR	22-APR-1998;	98US-0082797P.
			PR	28-APR-1998;	98US-0083322P.
			PR	28-APR-1998;	98US-0083495P.
			PR	29-APR-1998;	98US-0083496P.
Qy	1	MKLVTFILVITISLCSYSAFLINKVLPVDKLAFLPLDNLFPMDPLKLLKLTGLISV 60	PR	29-APR-1998;	98US-0083499P.
Db	1	MKLVTFILVITISLCSYSAFLINKVLPVDKLAFLPLDNLFPMDPLKLLKLTGLISV 60	PR	29-APR-1998;	98US-0083559P.
Qy	61	EHLVEGLKCKVNELGPEASEAVKKLEALSHLV 93	PR	05-MAY-1998;	98US-0084366P.
Db	61	EHLVEGLKCKVNELGPEASEAVKKLEALSHLV 93	PR	06-MAY-1998;	98US-0084414P.
RESULT 8			PR	07-MAY-1998;	98US-0084639P.
ID	ABU84384		PR	07-MAY-1998;	98US-0084640P.
XX	ABU84384 standard; protein; 93 AA.		PR	07-MAY-1998;	98US-0084643P.
AC	ABU84384;		PR	15-MAY-1998;	98US-0085579P.
XX			PR	15-MAY-1998;	98US-0085580P.
DT	02-AUG-2003 (first entry)		PR	15-MAY-1998;	98US-0085700P.
DE	Human secreted/transmembrane protein (PRO) #122.		PR	18-MAY-1998;	98US-0086023P.
XX			PR	22-MAY-1998;	98US-0086332P.
KW	Human; secreted and transmembrane protein; PRO; TNF-alpha;		PR	22-MAY-1998;	98US-0086486P.
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		PR	28-MAY-1998;	98US-0087098P.
KW	tissue typing.		PR	28-MAY-1998;	98US-0087208P.
XX			PR	02-JUN-1998;	98US-0087599P.
OS	Homo sapiens.		PR	02-JUN-1998;	98US-0087759P.
XX			PR	03-JUN-1998;	98US-0087827P.
XX	US2003032112-A1.		PR	04-JUN-1998;	98US-0088025P.
PD	13-FEB-2003.		PR	04-JUN-1998;	98US-0088028P.
XX			PR	04-JUN-1998;	98US-0088029P.
XX	21-JUN-2002; 2002US-00176756.		PR	04-JUN-1998;	98US-0088033P.
XX			PR	04-JUN-1998;	98US-0088326P.
PR	18-SEP-1997;	97US-0059263P.	PR	05-JUN-1998;	98US-0088167P.
PR	18-SEP-1997;	97US-0059266P.	PR	05-JUN-1998;	98US-0088202P.
PR	17-OCT-1997;	97US-0062250P.	PR	05-JUN-1998;	98US-0088212P.
PR	21-OCT-1997;	97US-0063486P.	PR	05-JUN-1998;	98US-0088217P.
PR	24-OCT-1997;	97US-0063120P.	PR	09-JUN-1998;	98US-0088655P.
PR	24-OCT-1997;	97US-0063121P.	PR	10-JUN-1998;	98US-0088722P.
PR	28-OCT-1997;	97US-0063540P.	PR	10-JUN-1998;	98US-0088738P.
PR	28-OCT-1997;	97US-0063541P.	PR	10-JUN-1998;	98US-0088740P.
PR	28-OCT-1997;	97US-0063544P.	PR	10-JUN-1998;	98US-0088811P.
PR	28-OCT-1997;	97US-0063564P.	PR	10-JUN-1998;	98US-0088824P.
PR	29-OCT-1997;	97US-0063734P.	PR	10-JUN-1998;	98US-0088825P.
PR	31-OCT-1997;	97US-0063870P.	PR	10-JUN-1998;	98US-0088826P.
PR	31-OCT-1997;	97US-0064103P.	PR	11-JUN-1998;	98US-0088861P.
PR	13-NOV-1997;	97US-0065311P.	PR	11-JUN-1998;	98US-0088863P.
PR	21-NOV-1997;	97US-0066120P.	PR	11-JUN-1998;	98US-0088876P.
PR	24-NOV-1997;	97US-0066466P.	PR	12-JUN-1998;	98US-0089090P.
PR	24-NOV-1997;	97US-0066772P.	PR	12-JUN-1998;	98US-0089105P.
PR	11-DEC-1997;	97US-0069335P.	PR	16-JUN-1998;	98US-0089512P.
PR	12-DEC-1997;	97US-0069425P.	PR	16-JUN-1998;	98US-0089514P.
PR	17-DEC-1997;	97US-0069870P.	PR	17-JUN-1998;	98US-0089538P.

PR 22-JUN-1998;	98US-0090254P.
PR 24-JUN-1998;	98US-0090429P.
PR 24-JUN-1998;	98US-0090433P.
PR 24-JUN-1998;	98US-0090444P.
PR 24-JUN-1998;	98US-0090461P.
PR 24-JUN-1998;	98US-0090535P.
PR 24-JUN-1998;	98US-0090549P.
PR 25-JUN-1998;	98US-0090676P.
PR 25-JUN-1998;	98US-0090678P.
PR 25-JUN-1998;	98US-0090688P.
PR 25-JUN-1998;	98US-0090690P.
PR 25-JUN-1998;	98US-0090694P.
PR 25-JUN-1998;	98US-0090695P.
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PR 26-JUN-1998;	98US-0010541P.
PR 26-JUN-1998;	98US-0090862P.
PR 26-JUN-1998;	98US-0090863P.
PR 26-JUN-1998;	98US-0091010P.
PR 01-JUL-1998;	98US-0091359P.
PR 01-JUL-1998;	98US-0091544P.
PR 02-JUL-1998;	98US-0091478P.
PR 02-JUL-1998;	98US-0091486P.
PR 02-JUL-1998;	98US-0091626P.
PR 02-JUL-1998;	98US-0091628P.
PR 02-JUL-1998;	98US-0091632P.
PR 24-JUL-1998;	98US-0094006P.
PR 04-AUG-1998;	98US-0095282P.
PR 10-AUG-1998;	98US-0095998P.
PR 10-AUG-1998;	98US-0096012P.
PR 17-AUG-1998;	98US-0096757P.
PR 17-AUG-1998;	98US-0096766P.
PR 17-AUG-1998;	98US-0096867P.
PR 17-AUG-1998;	98US-0096891P.
PR 17-AUG-1998;	98US-0096949P.
PR 18-AUG-1998;	98US-0096959P.
PR 18-AUG-1998;	98US-0097022P.
PR 26-AUG-1998;	98US-0097952P.
PR 26-AUG-1998;	98US-0097954P.
PR 26-AUG-1998;	98US-0097955P.
PR 26-AUG-1998;	98US-0097971P.
PR 26-AUG-1998;	98US-0097974P.
PR 26-AUG-1998;	98US-0098014P.
PR 01-SEP-1998;	98US-0098716P.
PR 01-SEP-1998;	98US-0098723P.
PR 02-SEP-1998;	98US-0098803P.
PR 02-SEP-1998;	98US-0098821P.
PR 02-SEP-1998;	98US-0098843P.
PR 09-SEP-1998;	98US-0099602P.
PR 10-SEP-1998;	98US-0099741P.
PR 10-SEP-1998;	98US-0099754P.
PR 10-SEP-1998;	98US-0099763P.
PR 10-SEP-1998;	98US-0099812P.
PR 15-SEP-1998;	98US-0100388P.
PR 16-SEP-1998;	98US-0100662P.
PR 16-SEP-1998;	98US-0100664P.
PR 16-SEP-1998;	98US-0101751P.
PR 16-SEP-1998;	98US-0101933P.
PR 17-SEP-1998;	98US-0100684P.
PR 17-SEP-1998;	98US-0100919P.
PR 17-SEP-1998;	98US-0100930P.
PR 18-SEP-1998;	98US-0100849P.
PR 18-SEP-1998;	98US-0101014P.
PR 18-SEP-1998;	98US-0101068P.
PR 23-SEP-1998;	98US-0101471P.
PR 23-SEP-1998;	98US-0101472P.
PR 23-SEP-1998;	98US-0101475P.
PR 23-SEP-1998;	98US-0101477P.
PR 23-SEP-1998;	98US-0101738P.
PR 24-SEP-1998;	98US-0101739P.
PR 24-SEP-1998;	98US-0101743P.
PR 24-SEP-1998;	98US-0101922P.
PR 25-SEP-1998;	98US-0101786P.
PR 29-SEP-1998;	98US-0102207P.
PR 29-SEP-1998;	98US-0102240P.
PR 29-SEP-1998;	98US-0102330P.
PR 29-SEP-1998;	98US-0102331P.
PR 29-SEP-1998;	98US-0102487P.
PR 30-SEP-1998;	98US-0102570P.
PR 30-SEP-1998;	98US-0102571P.
PR 01-OCT-1998;	98US-0102684P.
PR 01-OCT-1998;	98US-0102687P.
PR 02-OCT-1998;	98US-0102965P.
PR 06-OCT-1998;	98US-0103258P.
PR 06-OCT-1998;	98US-0103449P.
PR 07-OCT-1998;	98US-00168978.
Query Match 100.0%; Score 459; DB 6; Length 93;	
Best Local Similarity 100.0%; Pred. No. 5.6e-47;	
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MKLVTFLLVTISLCSYSATAPLINKVLPVDKLAFLPDNLPMDPKLLIKTLGTSV 60	
DB 1 MKLVTFLLVTISLCSYSATAPLINKVLPVDKLAFLPDNLPMDPKLLIKTLGTSV 60	
QY 61 EHLVEGLKRCVNELGPEASEAVKLEALSHLV 93	
DB 61 EHLVEGLKRCVNELGPEASEAVKLEALSHLV 93	
RESULT 9	
ABR66258	
ID ABR66258 standard; protein; 93 AA.	
XX AC ABR66258;	
XX DT 05-AUG-2003 (first entry)	
XX DE Human secreted polypeptide PRO1128, SEQ ID NO:244.	
XX KW Human; PRO; secreted protein; transmembrane protein;	
XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;	
XX KW chondrocyte; proliferation; differentiation; cartilage disorder;	
XX KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;	
XX KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;	
XX KW liver; drug screening; transgenic animal; genetic analysis;	
XX KW antiarthritic; vulnery; gene therapy.	
OS Homo sapiens.	
XX US2003027278-A1.	
XX PD 06-FEB-2003.	
XX PF 21-JUN-2002; 2002US-00176987.	
XX PR 18-SEP-1997; 97US-0059263P.	
XX PR 18-SEP-1997; 97US-0059266P.	
XX PR 17-OCT-1997; 97US-0062250P.	
XX PR 21-OCT-1997; 97US-0063486P.	
XX PR 24-OCT-1997; 97US-0063120P.	
XX PR 24-OCT-1997; 97US-0063121P.	
XX PR 28-OCT-1997; 97US-0063540P.	
XX PR 28-OCT-1997; 97US-0063541P.	
XX PR 28-OCT-1997; 97US-0063544P.	
XX PR 28-OCT-1997; 97US-0063564P.	
XX PR 29-OCT-1997; 97US-0063734P.	
XX PR 31-OCT-1997; 97US-0063870P.	
XX PR 31-OCT-1997; 97US-0064103P.	
XX PR 13-NOV-1997; 97US-0065311P.	
XX PR 21-NOV-1997; 97US-0066120P.	
XX PR 24-NOV-1997; 97US-0066466P.	
XX PR 24-NOV-1997; 97US-0066772P.	
XX PR 11-DEC-1997; 97US-0069335P.	
XX PR 12-DEC-1997; 97US-0069425P.	

PR	17-DEC-1997;	97US-0069870P.	PR	22-JUN-1998;	98US-0090252P.
PR	18-DEC-1997;	97US-0068017P.	PR	22-JUN-1998;	98US-0090254P.
PR	10-MAR-1998;	98US-0077450P.	PR	24-JUN-1998;	98US-0090429P.
PR	11-MAR-1998;	98US-0077632P.	PR	24-JUN-1998;	98US-0090435P.
PR	11-MAR-1998;	98US-0077649P.	PR	24-JUN-1998;	98US-0090444P.
PR	20-MAR-1998;	98US-0078886P.	PR	24-JUN-1998;	98US-0090461P.
PR	20-MAR-1998;	98US-0078939P.	PR	24-JUN-1998;	98US-0090535P.
PR	27-MAR-1998;	98US-0079664P.	PR	24-JUN-1998;	98US-0090540P.
PR	27-MAR-1998;	98US-0079786P.	PR	25-JUN-1998;	98US-0090676P.
PR	31-MAR-1998;	98US-0080107P.	PR	25-JUN-1998;	98US-0090678P.
PR	31-MAR-1998;	98US-0080194P.	PR	25-JUN-1998;	98US-0090688P.
PR	01-APR-1998;	98US-0080337P.	PR	25-JUN-1998;	98US-0090690P.
PR	01-APR-1998;	98US-0080333P.	PR	25-JUN-1998;	98US-0090694P.
PR	08-APR-1998;	98US-0081049P.	PR	25-JUN-1998;	98US-0090695P.
PR	08-APR-1998;	98US-0081070P.	PR	25-JUN-1998;	98US-0090696P.
PR	09-APR-1998;	98US-0081195P.	PR	26-JUN-1998;	98US-0090862P.
PR	15-APR-1998;	98US-0081838P.	PR	26-JUN-1998;	98US-0090863P.
PR	21-APR-1998;	98US-0082568P.	PR	26-JUN-1998;	98US-0090863P.
PR	21-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0091010P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-0091359P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-0091544P.
PR	28-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-0091478P.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0091486P.
PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0091626P.
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DT 05-AUG-2003 (first entry)
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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
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Db 61 EHLVEGLKRCVNLGPEASEAVKKLEALSHLV 93

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XX KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX KW chromosome mapping; gene mapping; cytostatic.
XX OS Homo sapiens.
XX PN US2003032113-A1.
XX PD 13-FEB-2003.
XX PF 20-JUN-2002; 2002US-00176911.
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PF 18-JUN-2002; 2002WO-US019456.
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PI Kimura S, Niimi T;
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WPI; 2003-184004/18.
XX
PT New human UGRP1 nucleic acid, useful for diagnosing or predicting a
PT predisposition to develop a respiratory disorder or determining the
PT prognosis of a subject having or suspected of having a respiratory
PT disorder e.g., asthma.
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PS Disclosure; Page 79; 83pp; English.
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CC The present invention provides the human and murine uteroglobin related
CC protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis
CC of and prediction of predisposition to respiratory disorders such as
CC asthma. The present sequence is a protein sequence shown in the
CC exemplification of the invention
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Query Match 100.0%; Score 459; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.6e-47;
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